



Nucleic Acids, Proteins, and Antibodies

Statement under 37 C.F.R. § 1.77(b)(4)

[1] This application refers to a "Sequence Listing" listed below, which is provided as an electronic document on two identical compact discs (CD-R), labeled "Copy 1" and "Copy 2." These compact discs each contain the following files, which are hereby incorporated in their entirety herein:

Document	File Name	Size in bytes	Date of Creation
Sequence Listing	PTZ32_seqList.txt	3,411,250	01/15/2001
V Viewer Setup File	SetupDLL.exe	695,808	12/19/2000
V Viewer Help File Controller	v.cnt	7,984	01/05/2001
V Viewer Program File	v.exe	753,664	12/19/2000
V Viewer Help File	v.hlp	447,766	01/05/2001

[2] The Sequence Listing may be viewed on an IBM-PC machine running the MS-Windows operating system by using the V viewer software, licensed by HGS, Inc., included on the compact discs (see World Wide Web URL: <http://www.fileviewer.com>).

Field of the Invention

[3] The present invention relates to novel proteins. More specifically, isolated nucleic acid molecules are provided encoding novel polypeptides. Novel polypeptides and antibodies that bind to these polypeptides are provided. Also provided are vectors, host cells, and recombinant and synthetic methods for producing human polynucleotides and/or polypeptides, and antibodies. The invention further relates to diagnostic and therapeutic

methods useful for diagnosing, treating, preventing and/or prognosing disorders related to these novel polypeptides. The invention further relates to screening methods for identifying agonists and antagonists of polynucleotides and polypeptides of the invention. The present invention further relates to methods and/or compositions for inhibiting or enhancing the production and function of the polypeptides of the present invention.

Background of the Invention

[4] One of the most critical tasks a cell must perform is to respond to cues from its environment, i.e., extracellular signals. Some of the most important extracellular signals come from other cells. The ability for cells to be able to send and receive signals from one another is of paramount importance in multicellular organisms because it allows individual cells within a body to become highly specialized and yet work in a coordinated fashion with other cells of the body. Cellular signaling mechanisms regulate a variety of cellular processes such as, for example, proliferation, differentiation, survival, movement, and secretion. Defects in cellular signaling can lead to a number of diseases and disorders such as cancers, immune system disorders and nervous system disorders. For more expansive reviews on this subject, please refer to Hunter, *Cell* 100:113-127 and Chapter 15 of *Molecular Biology of the Cell*, Third Edition, edited by Alberts et al. (1994), which are herein incorporated by reference in their entirety.

[5] Signal transduction requires molecules that serve as the extracellular signaling molecules as well as a set of receptors that "receive" the signal. Frequently, an additional set of proteins is necessary in order for the cell to translate the signal it has received into an appropriate response via the activation or inhibition of a particular set of genes or proteins. The signaling molecules, the receptor proteins, and the molecules that relay the signal between the receptor and the final effector molecules collectively form what are known as signal transduction pathways.

[6] To date, several common types of signal transduction pathways have been identified. One way to classify a signal transduction pathway is based on the class of receptor protein it utilizes. Two well known classes of receptor proteins are G-protein coupled receptors and enzyme-linked receptors. This latter class of enzyme-linked receptors includes receptor tyrosine kinases, tyrosine kinase associated receptors, receptor serine/threonine kinases, receptor tyrosine phosphatases, and receptor guanylyl cyclases.

Signal Transduction through G-protein Coupled Receptors

[7] G protein coupled receptors are the largest family of cell surface receptors. They are seven-pass transmembrane receptors which activate trimeric G proteins (G proteins) upon ligand binding. G proteins are GTPases composed of three subunits: alpha, beta and gamma. G proteins function as molecular switches existing in two states: an active GTP bound state and an inactive GDP bound state. Ligand binding to G protein coupled receptors induce inactive G proteins to release GDP allowing GTP to bind in its place. Binding of GTP to a G protein causes the alpha subunit to dissociate from the beta and gamma subunits which remain associated with one another. Eventually, the GTPase activity of the alpha subunit results in hydrolysis of the bound GTP molecule to GDP, thus inactivating the G protein.

[8] There are several types of G proteins that have been classified based upon their function. Stimulatory G proteins (G_s) are involved in adenylate cyclase activation; inhibitory G proteins (G_i) function to inhibit the activity of adenylate cyclase. Yet another type of G protein, G_q proteins, functions in the activation of phosphoinositide-specific phospholipase C enzyme.

[9] Activation of adenylate cyclase by an activated G_s protein results in the production of the cyclic nucleotide, cyclic AMP (cAMP). cAMP mediates its effects mostly through its activation of cAMP dependent kinase (A-kinase), a serine/threonine kinase. Activation of A-kinase helps to further relay the signal from the G protein coupled receptor to the target proteins. In muscle cells, for instance, activation of A-kinase following adrenaline signaling ultimately results in the activation of an enzyme, glycogen phosphorylase, which catalyzes the release of glucose molecules which can be used to produce energy from glycogen. In other instances, activated A-kinase translocates to the nucleus where it phosphorylates the cAMP response element binding (CREB) protein, which when phosphorylated, acts as a transcription factor to stimulate the expression of genes that have cAMP response elements (CRE) sequences in their regulatory regions.

[10] G_q proteins, when activated, activate the enzyme phospholipase C-beta which hydrolyzes PI 4,5-biphosphate (PIP_2) producing inositol triphosphate (IP_3) and diacylglycerol (DAG). IP_3 functions as a second messenger that causes the release of Ca^{2+} from intracellular stores. Released calcium then binds to Ca^{2+} binding proteins such as calmodulin, which in its calcium bound state, is able to activate Ca^{2+} /calmodulin dependent protein kinases (CaM-kinases). Activated CaM kinases then continue to relay the signal to

more downstream molecules in the signal transduction pathway. The other product produced by phospholipase C-beta, DAG, functions to activate the serine/threonine kinase known as protein kinase C (PKC). Activated PKC phosphorylates target proteins depending on the cell type, and in many cells these phosphorylation events lead to the increased transcription of specific genes. The highest concentrations of protein kinase C are found in the brain where PKC phosphorylates ion channels in nerve cells thereby altering their excitability. PKC activation can be induced by treating cells with phorbol esters which are able to cross the plasma membrane, bind to, and activate PKC directly.

Signal Transduction through Receptor Tyrosine Kinases

[11] The receptor protein tyrosine kinases (RPTKs) are some of the most well studied receptors, and the signaling cascades they initiate demonstrate two of the fundamental concepts in signal transduction: the regulation of protein phosphorylation and the recruitment of proteins into a signaling cascade via protein-protein interaction domains.

[12] Binding of the cognate ligand to a RPTK, such as epidermal growth factor (EGF) binding to the epidermal growth factor receptor (EGFR), induces RPTKs to dimerize and cross-phosphorylate each other on multiple tyrosine residues. The phosphorylated receptor dimer is the activated form of the receptor.

[13] The phosphorylated tyrosines on activated RPTKs are then recognized/bound by other components of the signal transduction pathway. One of the important discoveries in the field of signal transduction was the recognition of conserved domains which allow for protein-protein interactions in signaling pathways. The most prevalent binding domain that recognizes phosphotyrosine (P-Tyr) residues is known as the SH2 domain (for Src homology region 2, named after the Src protein in which the SH2 domain was first discovered). Another domain that recognizes P-Tyr residues is called the P-Tyr binding domain (PTB). The discovery of the SH2 domain was quickly followed by the discovery of several other protein-protein interaction domains involved in signal transduction and by the realization that most of these domains are modular in nature, meaning these domains fold independently – a most convenient feature for protein engineering. To date, more than 100 such protein interaction domains involved in signaling have been defined via comparative sequence analysis. Most of these domains recognize short linear sequences (approximately 4-10 amino acid residues in length), in some cases requiring phosphorylation of specific residues within the sequence allowing for inducible association. A convenient web based database, with

links to abstracts of papers characterizing these domains can be found at <http://smart.EMBL-Heidelberg.de>.

[14] Proteins containing SH2 and PTB domains translocate to the plasma membrane where they associate with the activated RPTKs which, in turn, activates them through phosphorylation. By way of example, activation of the platelet derived growth factor receptor (PDGFR) results in the autophosphorylation of tyrosine residues in the cytoplasmic tail of the PDGFR. These P-Tyr residues then serve as the binding sites for other proteins, such as a GTPase (discussed in more detail below), phospholipase C-gamma, and the regulatory subunit of PI-3-kinase, which are each able to recognize the P-Tyr residues in PDGFR via SH2 domains. The interaction of these proteins with the activated PDGFR results in the translocation of these proteins to the plasma membranes where they have their substrates and the PDGFR mediated activation of these proteins via phosphorylation.

[15] In the previous example, each of the proteins recruited to the activated RPTK via their SH2 domains also had catalytic activities that allowed them to propagate a signal. There are proteins involved in signal transduction, however, which have no ability in and of themselves to propagate a signal. Instead, these proteins, known as adaptor proteins, serve to couple activated RPTKs to other components of the signal transduction pathway which do have the capacity to propagate the signal. One such adaptor protein is known as Grb2. It contains one SH2 domain and two SH3 domains (another Src homology domain that mediates protein interactions). Grb 2 is constitutively associated with Sos protein, a guanine nucleotide releasing protein (GNRP), via its SH3 domain. Thus, when Grb2 associates with an activated receptor via its SH2 domain, it also brings Sos into proximity with the RPTK which activates the Sos protein via phosphorylation.

[16] GNRP proteins, such as Sos, are one of two types of proteins that help regulate the activity of proteins belonging to the Ras superfamily of monomeric GTPases. Ras proteins are proteins that are associated with the cytoplasmic side of the plasma membrane and help relay signals from RPTK to the nucleus to stimulate cell proliferation or differentiation. Ras proteins exist in two states, an inactive state in which ras is bound to GDP and an active state in which ras is bound to GTP. Activated GNRP proteins promote the exchange of bound GDP for GTP on ras proteins, thereby activating ras. Ras, itself, is a GTPase that hydrolyzes GTP to GDP, and would therefore tend to inactivate itself over time. However, ras is an inefficient GTPase, so the inactivation of ras is enhanced by GTPase activating proteins (GAPs) which increase the rate of hydrolysis of GTP by ras.

[17] Activated Ras kinases then act to activate more downstream signaling events, including activation of the mitogen-activated protein kinase (MAPK) pathway which is a cascade of serine/threonine kinases. Ras binds to and activates a MAPK kinase kinase (MAPKKK, such as Raf-1, for example), which in turn activates a MAPK kinase (MAPKK) via phosphorylation, which in turn activates a MAPK. MAPKs relay signals downstream by phosphorylating various proteins in the cell including other kinases and/or regulatory proteins in the cell. For instance, an activated MAPK can enter the nucleus and help to initiate transcription of genes that must be expressed in order for the cell to respond to the extracellular signal, such as genes required for DNA replication in response to the extracellular proliferation signal.

[18] Another class of signaling receptors, receptor serine/threonine kinases (RSK) has recently been identified. An example of an RSK is the TGF-beta receptor. Additionally, it has also been recently recognized that there are modular binding domains that recognize phosphoserine/phosphothreonine (P-Ser/P-Thr) residues. For instance, 14-3-3 domains recognize phosphoserines in specific amino acid contexts [RSX(P-Ser)XP] or [R(Y/F)X(P-Ser)XP] and may function in the assembly of signaling complexes. Other residues such as histidine and arginine can also be phosphorylated, and it is possible that additional kinases which phosphorylate these residues, or protein domains that bind phosphohistidine or phosphoarginine will be discovered.

Signaling Via Intracellular Receptors

[19] Some extracellular signals do not have cell surface receptors such as G protein coupled receptors or receptor tyrosine kinases. Instead, these extracellular signals are able to traverse the plasma membrane and interact with their receptors in the cytoplasm. Examples of such signals are the steroid hormones and the gas nitrous oxide (NO). The steroid hormone receptors, once bound by their ligand, are generally able to translocate to the nucleus where they bind regulatory DNA elements that control the gene expression of specific genes. NO gas, on the other hand, generally enters a cell and reacts with iron in the active site of the enzyme guanylate cyclase, stimulating it to produce cyclic GMP (cGMP). cGMP acts as a second messenger (similar to the way cAMP functions) and can stimulate further downstream signaling by binding to other proteins.

Terminating Signal Transduction

[20] As the effects of signal transduction are transient, there must also be mechanisms for terminating signal cascades. For example, G proteins are self-inactivating, and there are a set of proteins, GAPs, that are devoted to increasing the rate of hydrolysis of bound GTP by ras proteins. Cyclic nucleotide second messengers such as cAMP and cGMP are hydrolyzed by phosphodiesterases. In the case of kinases, there generally exist a set of complementary phosphatases that function to dephosphorylate phosphorylated residues, thereby bringing the signaling event to a close.

Signal Transduction Pathway Components and Disease

[21] Because signal transduction is involved in the regulation of so many cellular processes, including proliferation, differentiation, survival, and apoptosis, it is not surprising that defects in cellular signal transduction pathway components lead to a number of diseases and disorders, especially cancers. For a review on Signal transduction pathway components and diseases, see Hunter, Philosophical Transactions of the Royal Society of London Series B 353:583-605 (1998) which is herein incorporated by reference in its entirety. For instance, approximately 30% of human cancers have mutations in a ras gene, and at least 18 tyrosine kinases have been identified as oncogenes in either acutely transforming retroviruses or in human tumors, such as for example, Src. And more than 95% of chronic myelogenous leukemias express an activated form of the c-Abl non-receptor tyrosine kinases.

[22] Mutations in signaling pathways are also implicated in a plethora of other diseases. Mutation in Bruton's tyrosine kinase leads to X-linked agammaglobulinemia. Inactivation of ZAP70 or JAK3 leads to a severe combined immunodeficiency disease. Coffin-Lowry syndrome occurs when the X-linked Rsk2 protein serine kinase gene is inactivated. Myotonic dystrophy occurs when expression of the myotonic dystrophy serine kinase gene is decreased. Overexpression of the aurora2 serine kinase is implicated in colon carcinoma.

[23] The malfunction of signal transduction pathway components, particularly kinases, in diseases indicate that these genes are good targets for drugs/pharmaceuticals that either inhibit or activate their function. In fact, some such drugs have been developed and are already in use or in clinical trials. For instance, an inhibitor of cyclin dependent kinase 2 (cdk2), a kinase important in regulating cellular proliferation, is in clinical trials for cancer treatment, as are inhibitors of epidermal growth factor receptor tyrosine kinases and vascular endothelial growth factor receptor (VEGFR) tyrosine kinases. Inhibition of VEGFR activity

reduces or eliminates the vascularization of tumors directed by VEGFR. An antagonistic monoclonal antibody, herceptin, against the erbB2 receptor tyrosine kinase is being used in breast cancer therapies to treat breast cancers where ErbB2 is overexpressed.

[24] Thus there exists a clear need for identifying and exploiting novel signal transduction pathway component polynucleotides and polypeptides. Although structurally related, such proteins may possess diverse and multifaceted functions in a variety of cell and tissue types. The inventive purified signal transduction pathway component polypeptides are research tools useful for the identification, characterization and purification of additional proteins involved in signal transduction. Furthermore, the identification of new signal transduction pathway component polynucleotides and polypeptides permits the development of a range of derivatives, agonists and antagonists at the nucleic acid and protein levels which in turn have applications in the treatment and diagnosis of a range of conditions such as, for example, cancer and other proliferative disorders (e.g., chronic myelogenous leukemia), immunological disorders (e.g., severe combined immunodeficiency and X-linked agammaglobulinemia), and nervous system disorders (Coffin-Lowry Syndrome), amongst other conditions.

Summary of the Invention

[25] The present invention relates to novel proteins. More specifically, isolated nucleic acid molecules are provided encoding novel polypeptides. Novel polypeptides and antibodies that bind to these polypeptides are provided. Also provided are vectors, host cells, and recombinant and synthetic methods for producing human polynucleotides and/or polypeptides, and antibodies. The invention further relates to diagnostic and therapeutic methods useful for diagnosing, treating, preventing and/or prognosing disorders related to these novel polypeptides. The invention further relates to screening methods for identifying agonists and antagonists of polynucleotides and polypeptides of the invention. The present invention further relates to methods and/or compositions for inhibiting or enhancing the production and function of the polypeptides of the present invention.

Detailed Description

Tables

[26] Table 1A summarizes some of the polynucleotides encompassed by the invention (including cDNA clones related to the sequences (Clone ID NO:Z), contig sequences (contig identifier (Contig ID:)) and contig nucleotide sequence identifier (SEQ ID NO:X)) and further summarizes certain characteristics of these polynucleotides and the polypeptides encoded thereby. The first column provides the gene number in the application for each clone identifier. The second column provides a unique clone identifier, "Clone ID NO:Z", for a cDNA clone related to each contig sequence disclosed in Table 1A. The third column provides a unique contig identifier, "Contig ID:" for each of the contig sequences disclosed in Table 1A. The fourth column provides the sequence identifier, "SEQ ID NO:X", for each of the contig sequences disclosed in Table 1A. The fifth column, "ORF (From-To)", provides the location (i.e., nucleotide position numbers) within the polynucleotide sequence of SEQ ID NO:X that delineate the preferred open reading frame (ORF) that encodes the amino acid sequence shown in the sequence listing and referenced in Table 1A as SEQ ID NO:Y (column 6). Column 7 lists residues comprising predicted epitopes contained in the polypeptides encoded by each of the preferred ORFs (SEQ ID NO:Y). Identification of potential immunogenic regions was performed according to the method of Jameson and Wolf (CABIOS, 4; 181-186 (1988)); specifically, the Genetics Computer Group (GCG) implementation of this algorithm, embodied in the program PEPTIDESTRUCTURE (Wisconsin Package v10.0, Genetics Computer Group (GCG), Madison, Wisc.). This method returns a measure of the probability that a given residue is found on the surface of the protein. Regions where the antigenic index score is greater than 0.9 over at least 6 amino acids are indicated in Table 1A as "Predicted Epitopes". In particular embodiments, polypeptides of the invention comprise, or alternatively consist of, one, two, three, four, five or more of the predicted epitopes described in Table 1A. It will be appreciated that depending on the analytical criteria used to predict antigenic determinants, the exact address of the determinant may vary slightly. Column 8, "Tissue Distribution" shows the expression profile of tissue, cells, and/or cell line libraries which express the polynucleotides of the invention. The first number in column 8 (preceding the colon), represents the tissue/cell source identifier code corresponding to the key provided in Table 4. Expression of these polynucleotides was not observed in the other tissues and/or cell libraries tested. For those identifier codes in which the first two letters are not "AR", the second number in column 8 (following the colon), represents the number of times a sequence corresponding to the reference polynucleotide sequence (e.g., SEQ ID NO:X) was identified in the tissue/cell source. Those tissue/cell

source identifier codes in which the first two letters are "AR" designate information generated using DNA array technology. Utilizing this technology, cDNAs were amplified by PCR and then transferred, in duplicate, onto the array. Gene expression was assayed through hybridization of first strand cDNA probes to the DNA array. cDNA probes were generated from total RNA extracted from a variety of different tissues and cell lines. Probe synthesis was performed in the presence of ^{33}P dCTP, using oligo(dT) to prime reverse transcription. After hybridization, high stringency washing conditions were employed to remove non-specific hybrids from the array. The remaining signal, emanating from each gene target, was measured using a Phosphorimager. Gene expression was reported as Phosphor Stimulating Luminescence (PSL) which reflects the level of phosphor signal generated from the probe hybridized to each of the gene targets represented on the array. A local background signal subtraction was performed before the total signal generated from each array was used to normalize gene expression between the different hybridizations. The value presented after "[array code]:" represents the mean of the duplicate values, following background subtraction and probe normalization. One of skill in the art could routinely use this information to identify normal and/or diseased tissue(s) which show a predominant expression pattern of the corresponding polynucleotide of the invention or to identify polynucleotides which show predominant and/or specific tissue and/or cell expression. Column 9 provides the chromosomal location of polynucleotides corresponding to SEQ ID NO:X. Chromosomal location was determined by finding exact matches to EST and cDNA sequences contained in the NCBI (National Center for Biotechnology Information) UniGene database. Given a presumptive chromosomal location, disease locus association was determined by comparison with the Morbid Map, derived from Online Mendelian Inheritance in Man (Online Mendelian Inheritance in Man, OMIM™. McKusick-Nathans Institute for Genetic Medicine, Johns Hopkins University (Baltimore, MD) and National Center for Biotechnology Information, National Library of Medicine (Bethesda, MD) 2000. World Wide Web URL: <http://www.ncbi.nlm.nih.gov/omim/>). If the putative chromosomal location of the Query overlaps with the chromosomal location of a Morbid Map entry, an OMIM identification number is disclosed in column 10 labeled "OMIM Disease Reference(s)". A key to the OMIM reference identification numbers is provided in Table 5.

[27] Table 1B summarizes additional polynucleotides encompassed by the invention (including cDNA clones related to the sequences (Clone ID NO:Z), contig sequences (contig identifier (Contig ID:) contig nucleotide sequence identifiers (SEQ ID NO:X)), and genomic

sequences (SEQ ID NO:B). The first column provides a unique clone identifier, "Clone ID NO:Z", for a cDNA clone related to each contig sequence. The second column provides the sequence identifier, "SEQ ID NO:X", for each contig sequence. The third column provides a unique contig identifier, "Contig ID:" for each contig sequence. The fourth column, provides a BAC identifier "BAC ID NO:A" for the BAC clone referenced in the corresponding row of the table. The fifth column provides the nucleotide sequence identifier, "SEQ ID NO:B" for a fragment of the BAC clone identified in column four of the corresponding row of the table. The sixth column, "Exon From-To", provides the location (i.e., nucleotide position numbers) within the polynucleotide sequence of SEQ ID NO:B which delineate certain polynucleotides of the invention that are also exemplary members of polynucleotide sequences that encode polypeptides of the invention (e.g., polypeptides containing amino acid sequences encoded by the polynucleotide sequences delineated in column six, and fragments and variants thereof).

[28] Table 2 summarizes homology and features of some of the polypeptides of the invention. The first column provides a unique clone identifier, "Clone ID NO:Z", corresponding to a cDNA clone disclosed in Table 1A. The second column provides the unique contig identifier, "Contig ID:" corresponding to contigs in Table 1A and allowing for correlation with the information in Table 1A. The third column provides the sequence identifier, "SEQ ID NO:X", for the contig polynucleotide sequence. The fourth column provides the analysis method by which the homology/identity disclosed in the Table was determined. Comparisons were made between polypeptides encoded by the polynucleotides of the invention and either a non-redundant protein database (herein referred to as "NR"), or a database of protein families (herein referred to as "PFAM") as further described below. The fifth column provides a description of the PFAM/NR hit having a significant match to a polypeptide of the invention. Column six provides the accession number of the PFAM/NR hit disclosed in the fifth column. Column seven, "Score/Percent Identity", provides a quality score or the percent identity, of the hit disclosed in columns five and six. Columns 8 and 9, "NT From" and "NT To" respectively, delineate the polynucleotides in "SEQ ID NO:X" that encode a polypeptide having a significant match to the PFAM/NR database as disclosed in the fifth and sixth columns. In specific embodiments polypeptides of the invention comprise, or alternatively consist of, an amino acid sequence encoded by a polynucleotide in SEQ ID NO:X as delineated in columns 8 and 9, or fragments or variants thereof.

[29] Table 3 provides polynucleotide sequences that may be disclaimed according to

certain embodiments of the invention. The first column provides a unique clone identifier, "Clone ID", for a cDNA clone related to contig sequences disclosed in Table 1A. The second column provides the sequence identifier, "SEQ ID NO:X", for contig sequences disclosed in Table 1A. The third column provides the unique contig identifier, "Contig ID:", for contigs disclosed in Table 1A. The fourth column provides a unique integer 'a' where 'a' is any integer between 1 and the final nucleotide minus 15 of SEQ ID NO:X, and the fifth column provides a unique integer 'b' where 'b' is any integer between 15 and the final nucleotide of SEQ ID NO:X, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:X, and where b is greater than or equal to a + 14. For each of the polynucleotides shown as SEQ ID NO:X, the uniquely defined integers can be substituted into the general formula of a-b, and used to describe polynucleotides which may be preferably excluded from the invention. In certain embodiments, preferably excluded from the invention are at least one, two, three, four, five, ten, or more of the polynucleotide sequence(s) having the accession number(s) disclosed in the sixth column of this Table (including for example, published sequence in connection with a particular BAC clone). In further embodiments, preferably excluded from the invention are the specific polynucleotide sequence(s) contained in the clones corresponding to at least one, two, three, four, five, ten, or more of the available material having the accession numbers identified in the sixth column of this Table (including for example, the actual sequence contained in an identified BAC clone).

[30] Table 4 provides a key to the tissue/cell source identifier code disclosed in Table 1A, column 8. Column 1 provides the tissue/cell source identifier code disclosed in Table 1A, Column 8. Columns 2-5 provide a description of the tissue or cell source. Codes corresponding to diseased tissues are indicated in column 6 with the word "disease". The use of the word "disease" in column 6 is non-limiting. The tissue or cell source may be specific (e.g. a neoplasm), or may be disease-associated (e.g., a tissue sample from a normal portion of a diseased organ). Furthermore, tissues and/or cells lacking the "disease" designation may still be derived from sources directly or indirectly involved in a disease state or disorder, and therefore may have a further utility in that disease state or disorder. In numerous cases where the tissue/cell source is a library, column 7 identifies the vector used to generate the library.

[31] Table 5 provides a key to the OMIM reference identification numbers disclosed in Table 1A, column 10. OMIM reference identification numbers (Column 1) were derived from Online Mendelian Inheritance in Man (Online Mendelian Inheritance in Man, OMIM.

McKusick-Nathans Institute for Genetic Medicine, Johns Hopkins University (Baltimore, MD) and National Center for Biotechnology Information, National Library of Medicine, (Bethesda, MD) 2000. World Wide Web URL: <http://www.ncbi.nlm.nih.gov/omim/>). Column 2 provides diseases associated with the cytologic band disclosed in Table 1A, column 9, as determined using the Morbid Map database.

[32] Table 6 summarizes ATCC Deposits, Deposit dates, and ATCC designation numbers of deposits made with the ATCC in connection with the present application.

[33] Table 7 shows the cDNA libraries sequenced, and ATCC designation numbers and vector information relating to these cDNA libraries.

[34] Table 8 provides a physical characterization of clones encompassed by the invention. The first column provides the unique clone identifier, "Clone ID NO:Z", for certain cDNA clones of the invention, as described in Table 1A. The second column provides the size of the cDNA insert contained in the corresponding cDNA clone.

Definitions

[35] The following definitions are provided to facilitate understanding of certain terms used throughout this specification.

[36] In the present invention, "isolated" refers to material removed from its original environment (e.g., the natural environment if it is naturally occurring), and thus is altered "by the hand of man" from its natural state. For example, an isolated polynucleotide could be part of a vector or a composition of matter, or could be contained within a cell, and still be "isolated" because that vector, composition of matter, or particular cell is not the original environment of the polynucleotide. The term "isolated" does not refer to genomic or cDNA libraries, whole cell total or mRNA preparations, genomic DNA preparations (including those separated by electrophoresis and transferred onto blots), sheared whole cell genomic DNA preparations or other compositions where the art demonstrates no distinguishing features of the polynucleotide/sequences of the present invention.

[37] As used herein, a "polynucleotide" refers to a molecule having a nucleic acid sequence encoding SEQ ID NO:Y or a fragment or variant thereof; a nucleic acid sequence contained in SEQ ID NO:X (as described in column 3 of Table 1A) or the complement thereof; a cDNA sequence contained in Clone ID NO:Z (as described in column 2 of Table 1A and contained within a library deposited with the ATCC); a nucleotide sequence encoding

the polypeptide encoded by a nucleotide sequence in SEQ ID NO:B as defined in column 6 of Table 1B or a fragment or variant thereof; or a nucleotide coding sequence in SEQ ID NO:B as defined in column 6 of Table 1B or the complement thereof. For example, the polynucleotide can contain the nucleotide sequence of the full length cDNA sequence, including the 5' and 3' untranslated sequences, the coding region, as well as fragments, epitopes, domains, and variants of the nucleic acid sequence. Moreover, as used herein, a "polypeptide" refers to a molecule having an amino acid sequence encoded by a polynucleotide of the invention as broadly defined (obviously excluding poly-Phenylalanine or poly-Lysine peptide sequences which result from translation of a polyA tail of a sequence corresponding to a cDNA).

[38] In the present invention, "SEQ ID NO:X" was often generated by overlapping sequences contained in multiple clones (contig analysis). A representative clone containing all or most of the sequence for SEQ ID NO:X is deposited at Human Genome Sciences, Inc. (HGS) in a catalogued and archived library. As shown, for example, in column 2 of Table 1A, each clone is identified by a cDNA Clone ID (identifier generally referred to herein as Clone ID NO:Z). Each Clone ID is unique to an individual clone and the Clone ID is all the information needed to retrieve a given clone from the HGS library. Furthermore, certain clones disclosed in this application have been deposited with the ATCC on October 5, 2000, having the ATCC designation numbers PTA 2574 and PTA 2575; and on January 5, 2001, having the depositor reference numbers TS-1, TS-2, AC-1, and AC-2. In addition to the individual cDNA clone deposits, most of the cDNA libraries from which the clones were derived were deposited at the American Type Culture Collection (hereinafter "ATCC"). Table 7 provides a list of the deposited cDNA libraries. One can use the Clone ID NO:Z to determine the library source by reference to Tables 6 and 7. Table 7 lists the deposited cDNA libraries by name and links each library to an ATCC Deposit. Library names contain four characters, for example, "HTWE." The name of a cDNA clone (Clone ID) isolated from that library begins with the same four characters, for example "HTWEP07". As mentioned below, Table 1A correlates the Clone ID names with SEQ ID NO:X. Thus, starting with an SEQ ID NO:X, one can use Tables 1, 6 and 7 to determine the corresponding Clone ID, which library it came from and which ATCC deposit the library is contained in. Furthermore, it is possible to retrieve a given cDNA clone from the source library by techniques known in the art and described elsewhere herein. The ATCC is located at 10801 University Boulevard, Manassas, Virginia 20110-2209, USA. The ATCC deposits were made pursuant to the terms

of the Budapest Treaty on the international recognition of the deposit of microorganisms for the purposes of patent procedure.

[39] In specific embodiments, the polynucleotides of the invention are at least 15, at least 30, at least 50, at least 100, at least 125, at least 500, or at least 1000 continuous nucleotides but are less than or equal to 300 kb, 200 kb, 100 kb, 50 kb, 15 kb, 10 kb, 7.5kb, 5 kb, 2.5 kb, 2.0 kb, or 1 kb, in length. In a further embodiment, polynucleotides of the invention comprise a portion of the coding sequences, as disclosed herein, but do not comprise all or a portion of any intron. In another embodiment, the polynucleotides comprising coding sequences do not contain coding sequences of a genomic flanking gene (i.e., 5' or 3' to the gene of interest in the genome). In other embodiments, the polynucleotides of the invention do not contain the coding sequence of more than 1000, 500, 250, 100, 50, 25, 20, 15, 10, 5, 4, 3, 2, or 1 genomic flanking gene(s).

[40] A "polynucleotide" of the present invention also includes those polynucleotides capable of hybridizing, under stringent hybridization conditions, to sequences contained in SEQ ID NO:X, or the complement thereof (e.g., the complement of any one, two, three, four, or more of the polynucleotide fragments described herein), the polynucleotide sequence delineated in columns 8 and 9 of Table 2 or the complement thereof, and/or cDNA sequences contained in Clone ID NO:Z (e.g., the complement of any one, two, three, four, or more of the polynucleotide fragments, or the cDNA clone within the pool of cDNA clones deposited with the ATCC, described herein), and/or the polynucleotide sequence delineated in column 6 of Table 1B or the complement thereof. "Stringent hybridization conditions" refers to an overnight incubation at 42 degree C in a solution comprising 50% formamide, 5x SSC (750 mM NaCl, 75 mM trisodium citrate), 50 mM sodium phosphate (pH 7.6), 5x Denhardt's solution, 10% dextran sulfate, and 20 µg/ml denatured, sheared salmon sperm DNA, followed by washing the filters in 0.1x SSC at about 65 degree C.

[41] Also contemplated are nucleic acid molecules that hybridize to the polynucleotides of the present invention at lower stringency hybridization conditions. Changes in the stringency of hybridization and signal detection are primarily accomplished through the manipulation of formamide concentration (lower percentages of formamide result in lowered stringency); salt conditions, or temperature. For example, lower stringency conditions include an overnight incubation at 37 degree C in a solution comprising 6X SSPE (20X SSPE = 3M NaCl; 0.2M NaH₂PO₄; 0.02M EDTA, pH 7.4), 0.5% SDS, 30% formamide, 100 µg/ml salmon sperm blocking DNA; followed by washes at 50 degree C with 1XSSPE, 0.1% SDS.

In addition, to achieve even lower stringency, washes performed following stringent hybridization can be done at higher salt concentrations (e.g. 5X SSC).

[42] Note that variations in the above conditions may be accomplished through the inclusion and/or substitution of alternate blocking reagents used to suppress background in hybridization experiments. Typical blocking reagents include Denhardt's reagent, BLOTTO, heparin, denatured salmon sperm DNA, and commercially available proprietary formulations. The inclusion of specific blocking reagents may require modification of the hybridization conditions described above, due to problems with compatibility.

[43] Of course, a polynucleotide which hybridizes only to polyA⁺ sequences (such as any 3' terminal polyA⁺ tract of a cDNA shown in the sequence listing), or to a complementary stretch of T (or U) residues, would not be included in the definition of "polynucleotide," since such a polynucleotide would hybridize to any nucleic acid molecule containing a poly (A) stretch or the complement thereof (e.g., practically any double-stranded cDNA clone generated using oligo dT as a primer).

[44] The polynucleotide of the present invention can be composed of any polyribonucleotide or polydeoxribonucleotide, which may be unmodified RNA or DNA or modified RNA or DNA. For example, polynucleotides can be composed of single- and double-stranded DNA, DNA that is a mixture of single- and double-stranded regions, single- and double-stranded RNA, and RNA that is mixture of single- and double-stranded regions, hybrid molecules comprising DNA and RNA that may be single-stranded or, more typically, double-stranded or a mixture of single- and double-stranded regions. In addition, the polynucleotide can be composed of triple-stranded regions comprising RNA or DNA or both RNA and DNA. A polynucleotide may also contain one or more modified bases or DNA or RNA backbones modified for stability or for other reasons. "Modified" bases include, for example, tritylated bases and unusual bases such as inosine. A variety of modifications can be made to DNA and RNA; thus, "polynucleotide" embraces chemically, enzymatically, or metabolically modified forms.

[45] The polypeptide of the present invention can be composed of amino acids joined to each other by peptide bonds or modified peptide bonds, i.e., peptide isosteres, and may contain amino acids other than the 20 gene-encoded amino acids. The polypeptides may be modified by either natural processes, such as posttranslational processing, or by chemical modification techniques which are well known in the art. Such modifications are well described in basic texts and in more detailed monographs, as well as in a voluminous

research literature. Modifications can occur anywhere in a polypeptide, including the peptide backbone, the amino acid side-chains and the amino or carboxyl termini. It will be appreciated that the same type of modification may be present in the same or varying degrees at several sites in a given polypeptide. Also, a given polypeptide may contain many types of modifications. Polypeptides may be branched, for example, as a result of ubiquitination, and they may be cyclic, with or without branching. Cyclic, branched, and branched cyclic polypeptides may result from posttranslation natural processes or may be made by synthetic methods. Modifications include acetylation, acylation, ADP-ribosylation, amidation, covalent attachment of flavin, covalent attachment of a heme moiety, covalent attachment of a nucleotide or nucleotide derivative, covalent attachment of a lipid or lipid derivative, covalent attachment of phosphatidylinositol, cross-linking, cyclization, disulfide bond formation, demethylation, formation of covalent cross-links, formation of cysteine, formation of pyroglutamate, formylation, gamma-carboxylation, glycosylation, GPI anchor formation, hydroxylation, iodination, methylation, myristoylation, oxidation, pegylation, proteolytic processing, phosphorylation, prenylation, racemization, selenoylation, sulfation, transfer-RNA mediated addition of amino acids to proteins such as arginylation, and ubiquitination. (See, for instance, PROTEINS - STRUCTURE AND MOLECULAR PROPERTIES, 2nd Ed., T. E. Creighton, W. H. Freeman and Company, New York (1993); POSTTRANSLATIONAL COVALENT MODIFICATION OF PROTEINS, B. C. Johnson, Ed., Academic Press, New York, pgs. 1-12 (1983); Seifter et al., Meth. Enzymol. 182:626-646 (1990); Rattan et al., Ann. N.Y. Acad. Sci. 663:48-62 (1992)).

[46] "SEQ ID NO:X" refers to a polynucleotide sequence described, for example, in Tables 1A or 2, while "SEQ ID NO:Y" refers to a polypeptide sequence described in column 6 of Table 1A. SEQ ID NO:X is identified by an integer specified in column 4 of Table 1A. The polypeptide sequence SEQ ID NO:Y is a translated open reading frame (ORF) encoded by polynucleotide SEQ ID NO:X. "Clone ID NO:Z" refers to a cDNA clone described in column 2 of Table 1A.

[47] "A polypeptide having functional activity" refers to a polypeptide capable of displaying one or more known functional activities associated with a full-length (complete) protein. Such functional activities include, but are not limited to, biological activity, antigenicity [ability to bind (or compete with a polypeptide for binding) to an anti-polypeptide antibody], immunogenicity (ability to generate antibody which binds to a

specific polypeptide of the invention), ability to form multimers with polypeptides of the invention, and ability to bind to a receptor or ligand for a polypeptide.

[48] The polypeptides of the invention can be assayed for functional activity (e.g. biological activity) using or routinely modifying assays known in the art, as well as assays described herein. Specifically, one of skill in the art may routinely assay signal transduction pathway component polypeptides (including fragments and variants) of the invention for activity using assays as described in Examples 38, 39, 49, 52-57, 64 and 67.

[49] "A polypeptide having biological activity" refers to a polypeptide exhibiting activity similar to, but not necessarily identical to, an activity of a polypeptide of the present invention, including mature forms, as measured in a particular biological assay, with or without dose dependency. In the case where dose dependency does exist, it need not be identical to that of the polypeptide, but rather substantially similar to the dose-dependence in a given activity as compared to the polypeptide of the present invention (i.e., the candidate polypeptide will exhibit greater activity or not more than about 25-fold less and, preferably, not more than about tenfold less activity, and most preferably, not more than about three-fold less activity relative to the polypeptide of the present invention).

[50] Table 1A summarizes some of the polynucleotides encompassed by the invention (including contig sequences (SEQ ID NO:X) and clones (Clone ID NO:Z) and further summarizes certain characteristics of these polynucleotides and the polypeptides encoded thereby.

Polynucleotides and Polypeptides of the Invention

TABLE 1A

Gene No:	Clone ID NO: Z	Contig ID:	SEQ ID NO: X	ORF (From-To)	AA SEQ ID NO: Y	Predicted Epitopes	Tissue Distribution Library code: count (see Table IV for Library Codes)	Cytologic Band	OMIM Disease Reference(s):
1	HDPTE21	1165861	11	33 - 1790	624	Pro-16 to Gln-22, Arg-34 to Asn-41, Arg-49 to Lys-55, Leu-156 to Thr-163, Glu-169 to Glu-174, Ser-198 to Glu-214, Glu-246 to Pro-252, Arg-260 to Ser-271, Val-286 to Gly-291, Ser-304 to Glu-335, Pro-436 to Pro-451, Ser-482 to Gly-487, Val-498 to Ser-505, Asp-564 to Lys-585.	AR051: 26, AR050: 22, AR054: 21, AR089: 1, AR061: 1 H0529: 4, L0770: 4, L0748: 4, L0749: 3, L0777: 3, S0036: 2, L0756: 2, S0360: 1, H0036: 1, H0318: 1, H0457: 1, H0051: 1, H0328: 1, H0644: 1, S0002: 1, L0761: 1, L0766: 1, L0804: 1, L0784: 1, H0521: 1 and L0759: 1.		
						Gly-26 to Gly-32.			
2	H6EDR51	887711	443	1 - 639	1056		AR089: 1, AR061: 1 L0794: 11, L0777: 9,		
		901381	444	570 - 112	1057				
		1197894	12	1 - 1935	625	Glu-35 to Gln-44, Arg-70 to Val-77,			

6	HCE3E50	1227586	16	4 - 1650	629	Pro-1 to Ser-10, Pro-24 to Ser-29, Pro-43 to Glu-61.	L0774: 1, L0790: 1, L0663: 1, L0665: 1, H0345: 1, L0742: 1, L0748: 1, L0749: 1, H0707: 1, L0595: 1 and L0366: 1. AR061: 1, AR089: 1 H0521: 14, L0439: 6, L0754: 6, L0794: 4, L0748: 4, S0278: 3, L0766: 3, L0751: 3, L0747: 3, L0749: 3, H0556: 2, H0486: 2, H0250: 2, H0179: 2, H0271: 2, S0002: 2, S0426: 2, L0770: 2, L0769: 2, L0775: 2, L0659: 2, L0411: 1, S0134: 1, H0638: 1, S0418: 1, S0420: 1, S0354: 1, S0358: 1, S0360: 1, S0222: 1, H0613: 1, H0052: 1, H0051: 1, L0143: 1, L0455: 1, H0124: 1, H0090: 1, H0551: 1,			
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	H0333: 2, H0012: 2, T0010: 2, H0252: 2, H0063: 2, H0059: 2, S0002: 2, L0775: 2, L0655: 2, L0663: 2, L0665: 2, H0593: 2, H0658: 2, H0539: 2, H0555: 2, L0743: 2, L0744: 2, L0752: 2, L0731: 2, H0543: 2, H0624: 1, H0265: 1, H0650: 1, H0656: 1, S0212: 1, H0306: 1, H0305: 1, S0360: 1, S0046: 1, H0619: 1, S0222: 1, S6014: 1, H0613: 1, H0492: 1, H0250: 1, H0635: 1, H0427: 1, L0021: 1, H0036: 1, H0421: 1, H0399: 1, H0416: 1, H0188: 1, S0250: 1, L0143: 1, H0617: 1, H0673: 1, H0124: 1, H0163: 1, H0634: 1, H0087: 1, T0067: 1,					
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17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99 100

17	HHFJF24	1212624	27	1374 - 538	640	1.	Lys-1 to Ala-6, Ser-38 to Gln-43.	AR089: 1, AR061: 0 S0001: 1, H0619: 1, H0586: 1, H0427: 1 and L0595: 1.			
18	HHFMM10	910065	454	3 - 206	1067						
		1178801	28	368 - 751	641	Ser-19 to Thr-29, Lys-62 to Arg-67, Gln-102 to Phe-113.	AR089: 20, AR061: 7 H0031: 2, H0619: 1 and S0036: 1.				
		962997	455	95 - 493	1068	Gly-1 to Ser-13, Ile-24 to Phe-29.					
19	HHPBA42	901921	29	1 - 912	642	Gly-9 to Gln-15.	AR061: 133, AR089: 118 L0764: 4, L0659: 4, L0761: 3, S0360: 2, H0031: 2, L0662: 2, L0747: 2, L0750: 2, H0624: 1, H0295: 1, S0356: 1, S0132: 1, H0351: 1, L0394: 1, L0738: 1, H0051: 1, H0328: 1, L0796: 1, L0646: 1, L0800: 1, L0794: 1, L0549: 1, L0803: 1, L0806: 1, L0809: 1, L0788: 1,				

								L0789: 1, S0374: 1, H0435: 1, H0539: 1, S0378: 1, S0146: 1, L0754: 1, L0780: 1, L0752: 1 and L0591: 1.			
20	HHSP89	1217052	30	2 - 916	643	Gly-1 to Ile-11, Pro-49 to Asp-59, Val-64 to Leu-70, Gly-105 to Ser-112, Ser-130 to Ala-146, Asn-223 to Val-229, Asn-272 to Asp-278, Lys-294 to Tyr-305.		AR089: 1, AR061: 0 H0038: 3, H0616: 3, S0386: 2, L0366: 2, S0001: 1, S0360: 1, H0208: 1, S0046: 1, S6026: 1, H0486: 1, H0052: 1, H0201: 1, T0010: 1, S0036: 1, L0776: 1, S0216: 1, H0701: 1, H0593: 1, S0152: 1, H0521: 1, L0753: 1, L0758: 1 and S0031: 1.			
		910024	456	1 - 906	1069	Pro-46 to Asp-56, Val-61 to Leu-67, Gly-102 to Ser-109, Ser-127 to Ala-143, Asn-220 to Val-226.					
21	HKABX13	1167182	31	1 - 786	644	Lys-49 to Trp-55, Tyr-66 to Val-79, Arg-89 to Asp-106,		AR089: 12, AR061: 2 H0556: 1, H0250: 1, H0494: 1, L0809: 1 and			

					Gln-137 to Asn-142.	L0596: 1.			
	958656	457	2 - 763	1070	Pro-1 to Arg-15, Lys-49 to Trp-55, Tyr-66 to Val-79, Arg-89 to Asp-106, Gln-137 to Asn-142, Ala-171 to Tyr-178, Glu-224 to Ser-231.				
22	HLTHG77	1162409	32	2 - 406	645	Met-17 to Met-24, Ser-31 to Asp-37, Leu-70 to Asp-97.	AR089: 0, AR061: 0 S0192: 13, L0471: 4, H0051: 4, H0413: 4, L0779: 4, S0418: 3, S0388: 3, H0591: 3, L0666: 3, S0242: 3, S0414: 2, H0012: 2, H0040: 2, H0100: 2, S0422: 2, L0766: 2, L0663: 2, S0152: 2, L0748: 2, L0439: 2, L0591: 2, S0196: 2, H0170: 1, H0686: 1, S0134: 1, S0282: 1, S0356: 1, S0045: 1, S0222: 1, H0441: 1, H0587: 1, T0039: 1, H0263: 1, T0110: 1		

31	HPJCT50	909928	466	288 - 764	1079	Glu-48 to Leu-53.	L0809: 1, H0648: 1 and L0748: 1.		
		1201773	41	32 - 1567	654	Ser-3 to Trp-9, Arg-12 to Ser-18, Asp-42 to Gln-53, Arg-79 to Gly-90, Val-103 to Asp-108, Gly-175 to Asn-193, Ser-210 to Thr-217, Lys-242 to Glu-251, Glu-267 to Lys-273, Leu-287 to Lys-293, Ser-311 to Glu-318, Pro-335 to Lys-364, Asn-370 to Glu-376, Ala-392 to Thr-401.	AR089: 6, AR061: 4 H0561: 2, S0002: 2, H0521: 2, H0522: 2, H0656: 1, H0341: 1, H0550: 1, T0040: 1, H0036: 1, H0031: 1, H0560: 1, S0152: 1 and H0134: 1.		
		919836	467	32 - 1567	1080	Ser-3 to Trp-9, Arg-12 to Ser-18, Asp-42 to Gln-53, Arg-79 to Gly-90, Val-103 to Asp-108, Gly-175 to Asn-193, Ser-210 to Thr-217, Lys-242 to Glu-251, Glu-267 to Lys-273,			

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32	HPMFE91	1164740	42	605 - 1813	655	Leu-287 to Lys-293, Ser-311 to Glu-318, Pro-335 to Lys-364, Asn-370 to Glu-376, Ala-392 to Thr-401. Glu-6 to Asp-20, Thr-25 to Lys-31, Lys-73 to Ala-95, Glu-102 to Phe-109, Pro-112 to Pro-118, Asp-136 to Leu-152, Val-246 to Thr-253, Thr-298 to Glu-303, Val-312 to Arg-322, Pro-341 to Arg-349, Lys-378 to Phe-388, Val-392 to Ala-397.	AR061: 3, AR089: 2 L0766: 10, L0752: 8, L0439: 6, L0747: 6, L0740: 5, L0756: 5, L0779: 4, L0777: 4, L0731: 4, S0051: 3, L0803: 3, L0774: 3, L0754: 3, S0360: 2, H0574: 2, L0763: 2, L0805: 2, L0809: 2, L0663: 2, L0751: 2, L0755: 2, L0759: 2, L0601: 2, H0624: 1, S0040: 1, S0298: 1, S0420: 1, H0580: 1, H0351: 1, H0600: 1, H0331: 1, H0013: 1, L0021: 1, H0575: 1, H0590: 1, T0110: 1, H0012: 1, H0615: 1, H0031: 1, H0553: 1,		
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[illegible]

35	HSYCY88	914775	45	448 - 1089	658	<p>Leu-48 to Ser-55, Ser-63 to Ser-71, Asn-76 to Ala-82, Ser-87 to Phe-99, His-125 to Gly-140, Pro-160 to Asp-165.</p> <p>Gln-1 to Pro-29.</p>	<p>AR089: 2, AR061: 2 L0751: 11, L0747: 7, H0009: 5, L0659: 5, L0731: 5, S0046: 4, L0663: 4, H0392: 3, H0024: 3, H0124: 3, H0135: 3, L0500: 3, L0662: 3, L0508: 3, L0493: 3, L0779: 3, L0777: 3, L0758: 3, L0759: 3, S0360: 2, S0007: 2, H0208: 2, H0486: 2, H0012: 2, H0620: 2, H0264: 2, L0770: 2, L0769: 2, L0648: 2, L0775: 2, L0438: 2, L0744: 2, L0439: 2, L0749: 2, L0756: 2, S0260: 2, H0171: 1, S0040: 1,</p>		
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				S0420: 1, S0354: 1, S0045: 1, H0619: 1, H0549: 1, H0550: 1, H0592: 1, H0643: 1, H0427: 1, H0002: 1, H0599: 1, H0042: 1, H0575: 1, H0036: 1, H0590: 1, H0004: 1, H0618: 1, S0049: 1, H0597: 1, H0327: 1, H0150: 1, H0041: 1, L0471: 1, H0014: 1, H0051: 1, S6028: 1, S0250: 1, H0428: 1, H0622: 1, H0553: 1, H0644: 1, S0364: 1, H0551: 1, H0100: 1, S0112: 1, L0520: 1, L0502: 1, L0796: 1, L0771: 1, L0768: 1, L0497: 1, L0774: 1, L0378: 1, L0509: 1, L0776: 1, L0527: 1, L0515: 1, L0658: 1, L0809: 1, L0647: 1, L0790: 1, L0791: 1,				
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									L0792: 1, L0666: 1, L0664: 1, L0665: 1, H0520: 1, H0547: 1, H0519: 1, S0126: 1, H0690: 1, H0658: 1, H0672: 1, H0651: 1, S0378: 1, S0380: 1, H0521: 1, S0037: 1, S0028: 1, L0743: 1, L0740: 1, L0750: 1 and L0757: 1.			
36	HTEDW26	909749	46	3 - 959	659				AR061: 9, AR089: 9 H0521: 2, L0758: 2, H0038: 1, L0644: 1, L0645: 1, L0764: 1, L0662: 1, L0794: 1, L0557: 1, L0747: 1 and L0779: 1.			
37	HTEKD92	1090524	47	263 - 1165	660	Asn-11 to Pro-18, Tyr-31 to Asp-36, Asp-98 to Ser-119, Asp-142 to Glu-155, Gly-215 to Ile-226, Ser-237 to Ser-251, Leu-255 to Arg-260, His-263 to Asn-270.			AR089: 1, AR061: 1 L0805: 11, L0779: 7, L0803: 5, L0789: 5, L0776: 4, L0794: 3, L0777: 3, H0575: 2, H0687: 2, S0003: 2, S0214: 2, L0766: 2, L0747: 2, L0731: 2.			

									T0042: 1, L0764: 1, L0766: 1, L0653: 1, S0052: 1, H0144: 1, H0701: 1, L0777: 1, S0192: 1, H0542: 1 and H0543: 1.		
	909919	476	3 - 1151	1089	Arg-15 to Leu-23, Glu-70 to Lys-76, Lys-96 to Gln-102, Leu-119 to Arg-124, Ala-141 to Glu-146, Leu-159 to Glu-169, Thr-195 to Lys-202, Gln-239 to Gly-251.						
43	HWBCE37	906968	53	3 - 431	666				AR089: 1, AR061: 0 H0580: 1 and H0427: 1.		
44	HWLFB60	1223499	54	2 - 2233	667	Gly-1 to Lys-8, Arg-52 to Gly-57, Asp-69 to Ser-74, Arg-90 to Lys-97, Asp-126 to Thr-132, Cys-155 to Thr-171, Lys-189 to Ala-198, Lys-239 to Ser-245, Gln-260 to Ser-276,			AR089: 6, AR061: 0 L0766: 4, L0666: 4, L0439: 4, S0354: 3, H0014: 3, H0551: 3, H0529: 3, L0665: 3, H0519: 3, L0740: 3, L0759: 3, H0656: 2, S0003: 2, H0553: 2, L0775: 2, L0657: 2,		

HE6BK63 1153879 57 3 - 767 551 - 339 479 949702

47	HE6BK63	1153879	57	3 - 767	551 - 339	479	949702	Lys-1 to Thr-7, Arg-34 to Pro-41.	L0752: 2, L0755: 2, H0590: 1, H0014: 1, S0250: 1, L0772: 1, L0764: 1, L0804: 1, H0522: 1, S0406: 1, L0754: 1, L0779: 1, L0731: 1 and L0758: 1.		
								Gly-2 to Asp-11, Ser-71 to Gln-78, Ser-110 to Asn-117, Ser-155 to Ser-162, Thr-171 to Asp-181, Arg-193 to Leu-203, Arg-207 to Thr-215, Ala-225 to Lys-246, Lys-248 to Leu-255.	AR054: 21, AR050: 18, AR089: 17, AR051: 17, AR061: 14 H0090: 2, H0100: 2, L0792: 2, H0052: 1, H0012: 1, H0212: 1, S0426: 1, L0800: 1, L0663: 1, L0743: 1, L0756: 1 and L0780: 1.		
661045			480	586 - 1191	1093			Ser-12 to Gln-19, Ser-51 to Asn-58, Ser-96 to Ser-103, Thr-112 to Asp-122, Arg-134 to Leu-144, Arg-148 to Thr-156, Ala-166 to Lys-187, Lys-189 to Gly-200.			

51	HADFK69	1091937	61	201 - 782	674	Gln-74 to Gln-85. Glu-1 to Gly-6, Glu-50 to Val-55, Tyr-62 to Leu-67, Glu-105 to Lys-113, Ser-127 to Val-132, Ala-141 to Val-146, Thr-154 to Leu-159, Leu-170 to Ser-177, Pro-182 to Asn-194.	AR089: 4, AR061: 1 L0794: 3, L0803: 3, L0809: 3, S0222: 2, L0747: 2, L0756: 2, L0752: 2, L0758: 2, H0171: 1, L0002: 1, S0420: 1, S6026: 1, H0427: 1, L0021: 1, H0051: 1, T0010: 1, H0032: 1, S0422: 1, L0775: 1, L0659: 1, L0367: 1, L0790: 1, L0666: 1, L0744: 1, L0754: 1, L0779: 1, L0777: 1 and L0757: 1.		
52	HDPMO62	912850 1152329	484 62	1 - 573 1 - 447	1097 675	Gly-38 to Pro-48, Pro-105 to Ser-116, Arg-120 to Ser-127, Ser-142 to Ser-149. Ala-14 to Gly-20, Gly-34 to Pro-44, His-128 to Ser-134.	AR089: 1 S0002: 2 and H0522: 1.		
53	HDPMO85	912722 1228282	485 63	1 - 582 138 - 719	1098 676	Glu-58 to Ala-72, Thr-91 to Gln-98,	AR089: 8, AR061: 2 L0759: 15, L0766: 9,		

L0545: 2, L0666: 2,
L0665: 2, H0520: 2,
H0435: 2, H0522: 2,
H0576: 2, S0028: 2,
L0749: 2, L0756: 2,
L0753: 2, L0601: 2,
L0603: 2, H0265: 1,
S0114: 1, S0116: 1,
S0212: 1, H0402: 1,
S0418: 1, S0420: 1,
H0340: 1, H0489: 1,
S0045: 1, S0222: 1,
H0370: 1, H0486: 1,
T0109: 1, H0427: 1,
H0036: 1, S0010: 1,
L0563: 1, H0263: 1,
H0597: 1, H0545: 1,
H0150: 1, H0009: 1,
H0123: 1, H0050: 1,
L0471: 1, H0024: 1,
S0214: 1, H0604: 1,
H0030: 1, H0031: 1,
L0055: 1, H0124: 1,
S0366: 1, H0551: 1,
H0477: 1, H0487: 1,
H0268: 1, H0623: 1,

1. 2. 3. 4. 5. 6. 7. 8. 9. 10. 11. 12. 13. 14. 15. 16. 17. 18. 19. 20. 21. 22. 23. 24. 25. 26. 27. 28. 29. 30. 31. 32. 33. 34. 35. 36. 37. 38. 39. 40. 41. 42. 43. 44. 45. 46. 47. 48. 49. 50. 51. 52. 53. 54. 55. 56. 57. 58. 59. 60. 61. 62. 63. 64. 65. 66. 67. 68. 69. 70. 71. 72. 73. 74. 75. 76. 77. 78. 79. 80. 81. 82. 83. 84. 85. 86. 87. 88. 89. 90. 91. 92. 93. 94. 95. 96. 97. 98. 99. 100.

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|----|---------|---------|----|---------|-----|---|---|--|--|
| 54 | HDPUY72 | 1228285 | 64 | 2 - 595 | 677 | Tyr-63 to Ala-72,
Thr-91 to Gln-98,
Glu-106 to Glu-115,
Gln-128 to Asp-134,
Lys-143 to Lys-148,
Lys-170 to Ser-178,
Ser-183 to Gly-190.
Arg-1 to Pro-12,
Pro-18 to Lys-25,
Arg-28 to Cys-38,
Val-61 to Leu-67,
Pro-84 to Ser-95. | AR089: 7, AR061: 3
L0747: 17, L0439: 16,
H0556: 12, L0731: 11,
L0438: 10, L0740: 9,
L0754: 8, L0596: 7,
H0013: 6, L0659: 6,
H0521: 6, S0278: 5,
H0575: 5, S0126: 5,
S3014: 5, L0755: 5,
S0007: 4, S0003: 4,
H0622: 4, H0673: 4,
L0766: 4, L0803: 4,
L0775: 4, L0666: 4,
S0044: 4, L0748: 4,
L0759: 4, L0599: 4,
H0543: 4, S0358: 3,
H0574: 3, H0178: 3,
H0024: 3, H0051: 3,
H0266: 3, S0214: 3, | | |
|----|---------|---------|----|---------|-----|---|---|--|--|

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|--|--|--|--|--|--|--|--|
| | | | | | | H0551: 3, H0412: 3,
H0646: 3, L0598: 3,
L0764: 3, L0805: 3,
L0655: 3, L0517: 3,
H0547: 3, L0779: 3,
L0758: 3, H0170: 2,
S0040: 2, H0305: 2,
H0580: 2, H0299: 2,
H0600: 2, H0250: 2,
S0010: 2, H0052: 2,
H0263: 2, H0046: 2,
L0163: 2, S0051: 2,
T0010: 2, L0483: 2,
H0031: 2, H0032: 2,
S0036: 2, H0591: 2,
H0634: 2, T0067: 2,
H0264: 2, H0433: 2,
T0041: 2, S0144: 2,
S0142: 2, L0770: 2,
L0769: 2, L0771: 2,
L0774: 2, L0653: 2,
L0776: 2, L0664: 2,
L0565: 2, H0670: 2,
H0672: 2, S0152: 2,
S0404: 2, S0028: 2,
L0744: 2, L0745: 2, | |
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| | | | | | H0375: 1, H0594: 1,
H0687: 1, H0553: 1,
H0644: 1, L0055: 1,
H0383: 1, H0169: 1,
H0064: 1, H0708: 1,
H0068: 1, H0598: 1,
H0135: 1, H0038: 1,
H0616: 1, H0413: 1,
H0056: 1, S0112: 1,
L0564: 1, H0280: 1,
H0494: 1, H0625: 1,
H0561: 1, S0344: 1,
H0538: 1, L0763: 1,
L0761: 1, L0772: 1,
L0646: 1, L0800: 1,
L0773: 1, L0662: 1,
L0794: 1, L0650: 1,
L0651: 1, L0806: 1,
L0654: 1, L0528: 1,
L0663: 1, H0144: 1,
S0374: 1, H0520: 1,
H0682: 1, H0659: 1,
H0660: 1, H0648: 1,
S0328: 1, S0330: 1,
H0539: 1, S0380: 1,
H0518: 1, S0146: 1, |
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|----|---------|---------|----|-----------|-----|--|---|--|--|
| 56 | HE8TB94 | 1178794 | 66 | 470 -1087 | 679 | Ser-95 to Gly-103,
Thr-114 to Asn-120.

Gln-6 to Asp-13,
Thr-68 to Leu-80,
Arg-130 to Thr-135,
Pro-189 to Ser-201. | AR089: 2, AR061: 1
L0747: 10, H0266: 6,
H0623: 6, L0740: 5,
S0045: 3, H0050: 3,
H0551: 3, L0777: 3,
L0757: 3, L0759: 3,
L0588: 3, H0056: 2,
S0404: 2, L0745: 2,
L0780: 2, L0589: 2,
H0624: 1, H0170: 1,
S0360: 1, H0329: 1,
H0645: 1, H0437: 1,
H0601: 1, H0486: 1,
H0013: 1, H0123: 1,
L0471: 1, H0328: 1,
H0622: 1, H0591: 1,
H0433: 1, H0413: 1,
H0100: 1, S0210: 1,
L0769: 1, L0659: 1,
L0788: 1, S0126: 1,
S0044: 1, S0146: 1,
H0555: 1, S0037: 1,
S0027: 1, L0748: 1,
L0439: 1 and L0465: 1. | | |
|----|---------|---------|----|-----------|-----|--|---|--|--|

HEBGA65 1178633 68 309-977 1103 Glu-37 to Thr-42.
Lys-35 to Val-45,
Ser-133 to Ala-138,
Asp-162 to Asp-174,
Gln-179 to Cys-186,
Arg-214 to Pro-223.

| | | | | | | | | | |
|----|---------|---------|-----|-----------|------|---|--|--|--|
| 58 | HEBGA65 | 912932 | 490 | 164 - 688 | 1103 | Glu-37 to Thr-42. | H0579: 1, S0454: 1,
S0404: 1, L0745: 1,
S0260: 1, H0445: 1,
H0595: 1, S0026: 1,
H0423: 1, H0422: 1 and
H0506: 1. | | |
| | | 1178633 | 68 | 309 - 977 | 681 | Lys-35 to Val-45,
Ser-133 to Ala-138,
Asp-162 to Asp-174,
Gln-179 to Cys-186,
Arg-214 to Pro-223. | AR089: 1, AR061: 0
L0748: 5, H0559: 3,
H0009: 3, H0318: 2,
H0581: 2, H0052: 2,
H0135: 2, H0494: 2,
L0770: 2, L0766: 2,
L0809: 2, L0789: 2,
L0439: 2, L0751: 2,
L0755: 2, L0758: 2,
L0604: 2, H0352: 2,
S0040: 1, H0583: 1,
H0671: 1, H0661: 1,
H0402: 1, S0360: 1,
S0007: 1, H0645: 1,
H0351: 1, H0392: 1,
H0587: 1, S0005: 1,
H0156: 1, L0021: 1,
H0545: 1, H0012: 1,
H0024: 1, L0183: 1, | | |

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|--------|-----|------------|------|---|
| 912815 | 491 | 412 - 1035 | 1104 | Ser-99 to Ala-104,
Asp-128 to Asp-140, |
| | | | | T0010: 1, H0271: 1,
H0188: 1, S0314: 1,
H0252: 1, H0644: 1,
H0316: 1, H0090: 1,
H0551: 1, T0042: 1,
H0625: 1, S0450: 1,
S0426: 1, L0769: 1,
L0637: 1, L0761: 1,
L0667: 1, L0764: 1,
L0771: 1, L0768: 1,
L0774: 1, L0775: 1,
L0806: 1, L0653: 1,
L0776: 1, L0783: 1,
L0545: 1, L0666: 1,
S0428: 1, S0053: 1,
S0216: 1, H0519: 1,
H0682: 1, H0683: 1,
H0658: 1, S0378: 1,
H0518: 1, H0696: 1,
H0478: 1, S0028: 1,
L0747: 1, L0749: 1,
L0750: 1, L0757: 1,
L0759: 1, S0031: 1 and
H0423: 1. |

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|----|---------|---------|-----|------------|------|---|---|--|--|--|
| 59 | HEGGB59 | 1197907 | 69 | 398 - 1078 | 682 | Thr-158 to Gly-163,
Gly-195 to Tyr-201.
Tyr-1 to Asp-11,
Asp-64 to His-73,
Ala-90 to Gly-100,
Ile-133 to Asn-138,
Val-195 to His-213. | AR061: 2, AR089: 2
L0731: 5, L0439: 4,
H0662: 2, H0369: 2,
L0105: 2, H0622: 2,
L0794: 2, L0803: 2,
L0804: 2, L0775: 2,
L0809: 2, H0547: 2,
L0754: 2, L0758: 2,
L0485: 2, H0484: 1,
S0360: 1, H0550: 1,
H0441: 1, H0392: 1,
H0031: 1, H0644: 1,
L0369: 1, L0662: 1,
L0768: 1, L0790: 1,
L0663: 1, L0664: 1,
S0126: 1, H0555: 1,
L0756: 1, L0589: 1,
L0592: 1, L0599: 1 and
H0506: 1. | | | |
| 60 | HELHC48 | 912601 | 492 | 265 - 645 | 1105 | Tyr-1 to Asp-11,
Asp-64 to His-73,
Ala-90 to Ile-96.
Ile-3 to Thr-11,
Asn-31 to Lys-40, | AR061: 2, AR089: 1
L0439: 22, L0770: 11, | | | |

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|--|--|--|--|--|--|--|--|--|--|
| | H0290: 1, H0039: 1,
H0213: 1, H0644: 1,
H0628: 1, L0055: 1,
H0674: 1, H0090: 1,
H0634: 1, H0551: 1,
H0264: 1, H0413: 1,
H0494: 1, H0560: 1,
H0625: 1, S0448: 1,
H0130: 1, H0633: 1,
S0142: 1, S0002: 1,
UNKWN: 1, L0369: 1,
L0640: 1, L0763: 1,
L0646: 1, L0764: 1,
L0773: 1, L0768: 1,
L0803: 1, L0774: 1,
L0526: 1, L0809: 1,
L0647: 1, H0701: 1,
S0374: 1, S0310: 1,
L0352: 1, H0682: 1,
H0660: 1, H0666: 1,
H0648: 1, S0328: 1,
H0539: 1, S0380: 1,
H0522: 1, S0146: 1,
S0404: 1, S3014: 1,
S0206: 1, L0740: 1,
L0751: 1, L0750: 1, | | | | | | | | |
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|----|---------|---------|-----|---------|------|--|--|--|--|--|--|--|--|
| | | | | | | | | | L0756: 1, L0777: 1,
L0599: 1, L0608: 1,
L0366: 1, S0011: 1,
H0653: 1, S0192: 1,
S0194: 1, H0543: 1 and
S0452: 1. | | | | |
| 61 | HEQQH90 | 1212646 | 71 | 3 - 680 | 684 | Arg-14 to Cys-25,
Ala-90 to Arg-96,
Ile-115 to Asp-122,
Lys-147 to Ser-152,
Ala-202 to Gln-208,
Asp-211 to Ser-221. | | | AR089: 4, AR061: 2
H0457: 11, H0052: 3,
H0580: 2, H0529: 2,
L0655: 2, L0748: 2,
L0439: 2, L0779: 2,
H0261: 1, H0486: 1,
L0021: 1, H0575: 1,
T0071: 1, H0194: 1,
L0579: 1, H0087: 1,
H0264: 1, T0041: 1,
H0695: 1, L0766: 1,
L0803: 1, L0775: 1,
L0758: 1 and H0422: 1. | | | | |
| | | 907532 | 493 | 1 - 666 | 1106 | Arg-10 to Cys-21. | | | | | | | |
| 62 | HFKHA18 | 1152242 | 72 | 1 - 690 | 685 | Gly-7 to Pro-13,
Cys-19 to Gly-25,
Phe-51 to Lys-61,
Ala-88 to Phe-93,
Leu-130 to Ser-136,
Ala-221 to Cys-228. | | | AR089: 4, AR061: 4
H0666: 12, S0358: 10,
H0620: 10, L0750: 8,
L0747: 7, L0731: 7,
H0135: 5, L0659: 5,
L0740: 5, L0757: 5, | | | | |

S0360: 4, H0123: 4,
S0022: 4, L0666: 4,
L0665: 4, S0028: 4,
L0748: 4, L0777: 4,
L0588: 4, H0265: 3,
S0420: 3, H0208: 3,
H0046: 3, H0024: 3
H0284: 3, H0100: 3,
L0650: 3, L0375: 3,
L0382: 3, H0651: 3,
L0755: 3, H0352: 3,
S0278: 2, H0592: 2,
H0333: 2, H0253: 2,
H0544: 2, H0545: 2,
H0081: 2, H0012: 2,
H0266: 2, H0286: 2,
H0252: 2, H0428: 2,
H0628: 2, H0551: 2,
S0210: 2, L0763: 2,
L0770: 2, L0774: 2,
L0518: 2, L0809: 2,
H0547: 2, H0682: 2,
H0670: 2, S0037: 2,
S0027: 2, L0751: 2,
L0752: 2, L0758: 2,
L0601: 2, H0668: 2,

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|----|---------|---------|-----|---------|------|--|---|---------|--|
| 64 | HHBFM91 | 1092116 | 74 | 3 - 506 | 687 | Ala-19 to Phe-24,
Thr-45 to Val-53,
Ile-77 to Arg-83,
Ser-105 to Gly-111,
Gln-128 to Ala-144,
Asp-153 to Gly-161. | S0031: 1.
AR089: 8, AR061: 1
H0575: 2, S0031: 2,
S0134: 1, H0156: 1,
H0373: 1, H0328: 1,
H0135: 1, S0428: 1,
H0682: 1, H0435: 1,
H0518: 1, H0521: 1,
L0779: 1 and L0758: 1. | | 264470 |
| | | 912832 | 495 | 2 - 343 | 1108 | | | | |
| 65 | HIBBF63 | 912715 | 75 | 3 - 419 | 688 | Thr-3 to Arg-10,
Lys-71 to Lys-80,
Glu-107 to Arg-120,
Lys-128 to Gly-133. | L0748: 2, H0052: 1,
H0194: 1, T0010: 1,
H0658: 1, S0380: 1 and
L0366: 1. | 16p13.3 | 141750,
141800,
141800,
141800,
141800,
141850,
141850,
141850,
141850,
141850,
156850,
186580,
191092,
600140,
600273,
601313, |

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| 66 | HMCEI38 | 1134410 | 76 | 190 - 627 | 689 | Gln-21 to Ala-28,
Tyr-55 to Phe-60,
Tyr-78 to Ile-84. | AR061: 4, AR089: 2
H0645: 1, H0494: 1,
S0142: 1, H0593: 1 and
H0435: 1. | | 601785 |
| | | 912580 | 496 | 189 - 626 | 1109 | Gln-21 to Ala-28,
Tyr-55 to Phe-60,
Tyr-78 to Ile-84. | | | |
| 67 | HMWJD68 | 1154790 | 77 | 1181 - 3 | 690 | Pro-7 to Ile-20,
Arg-26 to Trp-36,
Trp-68 to Thr-88,
Pro-96 to Gly-101,
Ser-109 to Arg-117,
Pro-163 to Ala-169,
Asp-260 to Asp-266. | AR061: 6, AR089: 5
H0641: 4, H0521: 4,
S0418: 2, H0617: 2,
L0794: 2, H0436: 2,
L0748: 2, L0596: 2,
H0556: 1, S0134: 1,
H0650: 1, H0657: 1,
H0341: 1, S0001: 1,
H0638: 1, S0358: 1,
S0045: 1, S0278: 1,
S0474: 1, H0545: 1,
H0081: 1, H0271: 1,
H0416: 1, H0551: 1,
H0623: 1, H0059: 1,
S0344: 1, L0761: 1,
L0803: 1, L0804: 1,
L0383: 1, H0435: 1,
S0152: 1, H0522: 1, | | |

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|----|---------|---------|----------|----------|---|--|--|--|--|--|
| | | | | | | | | L0749: 1, L0753: 1,
H0445: 1, H0595: 1 and
H0677: 1. | | |
| | 912628 | 497 | 14 - 685 | 1110 | Pro-2 to Cys-9,
Gly-27 to Glu-32,
Thr-87 to Asn-103,
Thr-146 to Lys-157,
Lys-189 to Val-194,
Lys-210 to Arg-218. | | | | | |
| 68 | HOEOL58 | 1078090 | 78 | 66 - 338 | 691 | Glu-11 to Asp-26,
Val-71 to Lys-87. | | AR089: 6, AR061: 5
S0126: 2, H0543: 2,
H0539: 1 and S0152: 1. | | |
| | 912836 | 498 | 3 - 407 | 1111 | | | | | | |
| 69 | HRACA51 | 1162856 | 79 | 3 - 677 | 692 | Asn-43 to Asn-50,
Ala-77 to Gly-92,
Thr-103 to Asn-109,
Gly-132 to Glu-142,
Ile-185 to Gly-196,
Arg-207 to Ser-214. | | AR089: 2, AR061: 1
L0777: 7, L0766: 5,
L0770: 4, L0769: 4,
L0803: 3, H0555: 3,
H0087: 2, L0761: 2,
L0809: 2, L0758: 2,
S6024: 1, H0650: 1,
H0580: 1, S0278: 1,
H0549: 1, S0222: 1,
H0586: 1, H0618: 1,
H0318: 1, H0597: 1,
H0546: 1, H0545: 1,
H0123: 1, H0014: 1. | | |

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| 70 | HSHAV32 | 912776 | 499 | 1 - 666 | 1112 | Asn-40 to Asn-47,
Ala-74 to Gly-89,
Thr-100 to Asn-106,
Gly-129 to Glu-139,
Ile-182 to Gly-193,
Arg-204 to Ser-211. | H0015: 1, H0107: 1,
H0083: 1, H0510: 1,
S6028: 1, H0252: 1,
H0622: 1, H0272: 1,
H0100: 1, H0494: 1,
S0144: 1, L0800: 1,
L0768: 1, L0794: 1,
L0804: 1, L0806: 1,
H0689: 1, H0672: 1,
S0328: 1, H0631: 1,
S0028: 1, L0749: 1,
L0750: 1, L0780: 1,
L0755: 1, L0759: 1,
S0434: 1, L0592: 1,
H0668: 1 and H0423: 1. | | |
| | | 1180388 | 80 | 157 - 627 | 693 | Phe-49 to Lys-55. | AR089: 4, AR061: 3
L0731: 7, L0749: 6,
L0105: 5, H0046: 5,
L0748: 5, H0551: 4,
L0747: 4 L0777: 4 | | |

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|----|---------|---------|-----|------------|------|--|--|--|---|--|--|
| 72 | HTPDV73 | 997659 | 82 | 423 - 118 | 695 | | | | H0435: 1, H0670: 1,
S0432: 1 and H0542: 1. | | |
| | | 912947 | 501 | 276 - 752 | 1114 | Asp-14 to Ile-20. | | | AR089: 0, AR061: 0
H0039: 2 | | |
| 73 | HTPHE33 | 1163871 | 83 | 1251 - 703 | 696 | Pro-10 to Gly-15,
Lys-80 to Ile-88,
Gly-161 to Tyr-169,
Arg-175 to Arg-183. | | | AR061: 0, AR089: 0
L0749: 5, H0622: 3,
L0731: 3, L0803: 2,
L0748: 2, L0777: 2,
S0134: 1, H0657: 1,
H0050: 1, S0048: 1,
S0036: 1, H0616: 1,
H0264: 1, H0488: 1,
L0663: 1 and H0659: 1. | | |
| | | 963658 | 502 | 852 - 1478 | 1115 | Gln-1 to Gly-13,
Thr-57 to Phe-63,
Gln-84 to Tyr-89,
Glu-98 to Pro-104,
Tyr-161 to Phe-168,
Leu-181 to Glu-202. | | | | | |
| 74 | HUFDN58 | 1224609 | 84 | 391 - 1071 | 697 | Tyr-1 to Asp-11,
Asp-64 to His-73,
Ala-90 to Gly-100,
Ile-133 to Asn-138,
Val-195 to His-213. | | | AR089: 3, AR061: 1
L0731: 5, L0439: 4,
H0662: 2, H0369: 2,
L0105: 2, H0622: 2,
L0794: 2, L0803: 2,
L0804: 2, L0775: 2, | | |

H0556: 1, H0686: 1,
 H0295: 1, H0341: 1,
 S0418: 1, S0376: 1,
 S0444: 1, H0580: 1,
 H0329: 1, S0468: 1,
 H0208: 1, S0045: 1,
 H0619: 1, L0717: 1,
 H0549: 1, H0550: 1,
 H0587: 1, L0021: 1,
 H0581: 1, H0309: 1,
 H0546: 1, H0457: 1,
 H0150: 1, H0041: 1,
 H0050: 1, H0024: 1,
 L0163: 1, H0266: 1,
 H0615: 1, H0688: 1,
 H0031: 1, H0628: 1,
 H0087: 1, H0334: 1,
 H0633: 1, S0210: 1,
 L0772: 1, L0643: 1,
 L0764: 1, L0662: 1,
 L0767: 1, L0775: 1,
 L0651: 1, L0806: 1,
 L0776: 1, L0656: 1,
 L0783: 1, L0383: 1,
 L0543: 1, L0789: 1,
 L0663: 1, H0547: 1,

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|----|---------|---------|-----|-----------|------|---|---|--|--|--|
| 79 | HWLKF25 | 912581 | 507 | 2 - 565 | 1120 | Arg-1 to Gln-15,
Thr-52 to His-57,
Ala-88 to Gln-99,
Ser-114 to His-121,
Val-129 to Gly-136. | Pro-334 to Glu-344,
Gln-382 to Pro-389. | L0646: 1, L0773: 1,
L0803: 1, L0375: 1,
L0651: 1, L0636: 1,
L0664: 1, H0522: 1,
L0439: 1, L0779: 1,
L0777: 1, L0731: 1 and
H0136: 1. | | |
| | | 1089052 | 89 | 224 - 886 | 702 | Val-49 to Gln-56,
Ala-85 to Leu-93,
Pro-96 to Ala-101,
Val-110 to Asn-118,
Asp-131 to Glu-136,
Lys-146 to Ala-159,
Met-164 to Tyr-169,
Thr-174 to Thr-180. | Val-49 to Gln-56,
Ala-85 to Leu-93,
Pro-96 to Ala-101,
Val-110 to Asn-118,
Asp-131 to Glu-136,
Lys-146 to Ala-159, | AR061: 3, AR089: 2
S0358: 1, H0052: 1,
L0803: 1 and L0759: 1. | | |
| | | 912842 | 508 | 224 - 889 | 1121 | Val-49 to Gln-56,
Ala-85 to Leu-93,
Pro-96 to Ala-101,
Val-110 to Asn-118,
Asp-131 to Glu-136,
Lys-146 to Ala-159, | | | | |

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|----|---------|---------|----|-------------|-----|--|---|--|--|
| 80 | H2CBH45 | 963811 | 90 | 2 - 421 | 703 | Met-164 to Tyr-169,
Thr-174 to Thr-180,
Ser-213 to Gly-218.

Ala-1 to Met-18,
Leu-20 to Asn-26,
Val-38 to Leu-46,
Pro-48 to Gly-53,
Leu-81 to Gly-86,
Gln-94 to Tyr-99,
Glu-101 to Gly-109. | AR061: 3, AR089: 3
H0437: 1, S0280: 1,
T0110: 1, H0622: 1,
L0745: 1, L0746: 1,
L0731: 1 and L0596: 1. | | |
| 81 | HAGDN53 | 1092161 | 91 | 2 - 430 | 704 | | AR050: 17, AR051:
11, AR054: 2, AR089:
1, AR061: 0
S0010: 1 and S0027: 1. | | |
| 82 | HAMFM39 | 971347 | 92 | 1121 - 2929 | 705 | Pro-9 to Gln-16,
Phe-31 to Tyr-40,
Gln-61 to Trp-66,
Arg-71 to Gln-78,
Gly-86 to Arg-92.

Gln-1 to Ala-7,
Thr-36 to Trp-42,
Gly-45 to Gly-52,
Glu-77 to Pro-89,
Gly-105 to Gly-132,
Ser-135 to Glu-162. | AR050: 193, AR054:
122, AR051: 84,
AR089: 0, AR061: 0
H0255: 59, H0254: 10,
H0617: 9, L0747: 8,
S0358: 7, H0486: 6,
L0655: 6, H0208: 4. | | |

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|----|---------|--------|----|---------|-----|---|--|---|--|--|
| 86 | HCECM90 | 945088 | 96 | 2 - 577 | 709 | Gly-12 to Gly-31,
Asn-38 to Gly-62,
Asp-70 to Phe-84,
Val-94 to Ser-101,
Ala-112 to Ser-125,
Lys-140 to Asn-145,
Asn-175 to Tyr-180,
Arg-187 to Thr-192. | AR061: 2, AR089: 1
H0013: 3, L0439: 2,
H0624: 1, H0171: 1,
S0040: 1, S0420: 1,
H0619: 1, H0156: 1,
H0575: 1, H0590: 1,
H0052: 1, H0011: 1,
H0266: 1, H0494: 1,
L0519: 1, H0519: 1,
H0555: 1, L0777: 1,
L0758: 1, S0436: 1 and
H0506: 1. | L0021: 1, H0581: 1,
S0049: 1, L0471: 1,
H0266: 1, L0351: 1,
L0772: 1, L0766: 1,
L0776: 1, L0659: 1,
L0792: 1, H0522: 1,
S0027: 1, L0779: 1 and
S0011: 1. | | |
| 87 | HCEPH71 | 522739 | 97 | 3 - 410 | 710 | Val-1 to Lys-8,
Pro-36 to Lys-41,
Gln-49 to Lys-57,
Ser-63 to Ser-70,
Asp-79 to Gln-92,
Asn-103 to Thr-122. | AR089: 1, AR061: 1
H0052: 1 and T0067:
1. | | | |

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|----|---------|---------|-----|----------|------|--|---|--|--|
| 88 | HCFMT57 | 1175204 | 98 | 3 - 1220 | 711 | Arg-4 to Val-12,
Glu-19 to Arg-29,
Glu-34 to Arg-76. | AR061: 0, AR089: 0
L0157: 2, H0620: 2,
L0666: 2, S0001: 1,
L0717: 1, H0549: 1,
S0222: 1, H0581: 1,
H0194: 1, H0015: 1,
H0399: 1, H0271: 1,
H0688: 1, H0428: 1,
H0124: 1, L0637: 1,
H0672: 1, L0439: 1,
L0750: 1 and H0423: 1. | | |
| | | 765375 | 511 | 380 - 3 | 1124 | Glu-5 to Arg-15,
Glu-20 to Arg-62. | | | |
| 89 | HCOMM05 | 1173146 | 99 | 3 - 851 | 712 | Glu-22 to Asp-41,
Pro-49 to Thr-58,
Leu-99 to Gly-107,
Ala-117 to Ala-122,
Gln-128 to Trp-134,
Pro-136 to Pro-144,
Phe-147 to Glu-153,
Glu-183 to Val-188,
Glu-195 to Glu-200,
Glu-257 to Leu-265,
Met-275 to Ser-283. | AR089: 1, AR061: 1
H0670: 1 | | |
| | | 925952 | 512 | 1 - 840 | 1125 | Gln-19 to Asp-38,
Pro-46 to Thr-55, | | | |

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|----|---------|--------|-----|-----------|-----|--|---|--|--|
| 94 | HDPFF24 | 909232 | 104 | 104 - 460 | 717 | | L0779: 1, L0759: 1 and
H0543: 1. | | |
| | | | | | | | AR089: 4, AR061: 1
H0171: 5, S0026: 3,
S0400: 2, L0471: 2,
H0031: 2, H0553: 2,
H0547: 2, H0521: 2,
L0759: 2, H0423: 2,
H0170: 1, H0583: 1,
H0656: 1, S0001: 1,
S0358: 1, S0360: 1,
H0244: 1, H0349: 1,
H0590: 1, H0310: 1,
H0014: 1, H0039: 1,
S0366: 1, H0551: 1,
L0351: 1, H0509: 1,
S0150: 1, L0369: 1,
L0796: 1, L0773: 1,
L0662: 1, L0766: 1,
L0803: 1, L0635: 1,
L0540: 1, H0519: 1,
H0684: 1, H0660: 1,
H0666: 1, S0044: 1,
H0478: 1, H0479: 1,
H0626: 1, L0748: 1,
L0740: 1, L0777: 1, | | |

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|----|---------|---------|-----|---------|------|---|--|--|--|
| 98 | HE6GF02 | 1150897 | 108 | 804 - 1 | 721 | Gln-13 to Ser-18,
Glu-32 to Gly-37,
Ala-44 to Trp-49,
Glu-56 to Val-61,
Gln-68 to Lys-74,
Ala-83 to Glu-88,
Arg-111 to Gly-117,
Tyr-123 to His-143,
Ser-167 to Thr-202. | H0543: 1.
AR061: 7, AR089: 4
H0100: 1 and H0521:
1. | | |
| | | 911263 | 514 | 1 - 264 | 1127 | Gln-13 to Ser-18,
Glu-32 to Gly-37,
Ala-44 to Trp-49. | | | |
| 99 | HE8PK12 | 909884 | 109 | 2 - 367 | 722 | Val-30 to Ser-37,
Gln-43 to Asp-62,
Pro-74 to Glu-79,
Thr-102 to Phe-109. | AR089: 6, AR061: 4
L0754: 6, L0777: 6,
L0740: 5, L0731: 4,
L0758: 4, L0759: 4,
S0001: 3, S0280: 3,
L0770: 3, L0764: 3,
L0747: 3, L0749: 3,
L0366: 3, S0412: 3,
S0007: 2, H0411: 2,
H0013: 2, L0471: 2,
T0004: 2, L0598: 2,
L0638: 2, L0662: 2,
L0783: 2, L0438: 2, | | |

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|-----|---------|--------|-----|----------|------|---|---|---------------------|--|
| 102 | HFBDJ13 | 911264 | 515 | 85 - 486 | 1128 | Gly-11 to Thr-16,
Ser-35 to Ser-56,
Thr-58 to Ser-73,
Tyr-85 to Asp-91,
Glu-100 to Glu-109. | H0024: 1, T0010: 1,
H0510: 1, H0644: 1,
S0036: 1, H0551: 1,
H0264: 1, H0488: 1,
H0056: 1, H0100: 1,
L0564: 1, T0041: 1,
H0652: 1, S0344: 1,
S0002: 1, L0763: 1,
L0638: 1, L0761: 1,
L0372: 1, L0643: 1,
L0764: 1, L0768: 1,
L0381: 1, L0775: 1,
L0526: 1, L0782: 1,
L0663: 1, L0665: 1,
H0703: 1, H0520: 1,
H0435: 1, H0521: 1,
S0044: 1, L0751: 1,
L0757: 1, L0759: 1,
H0445: 1, L0584: 1,
L0608: 1 and H0506: 1. | S0007: 2, L0794: 2, | |
|-----|---------|--------|-----|----------|------|---|---|---------------------|--|

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| | | | | | L0617: 1, S0358: 1,
H0609: 1, H0592: 1,
H0333: 1, T0040: 1,
H0013: 1, H0635: 1,
H0575: 1, H0036: 1,
H0581: 1, H0123: 1,
H0050: 1, H0012: 1,
H0071: 1, T0010: 1,
H0687: 1, H0290: 1,
H0617: 1, H0606: 1,
H0038: 1, H0487: 1,
H0494: 1, H0334: 1,
S0150: 1, H0647: 1,
S0142: 1, L0640: 1,
L0639: 1, L0637: 1,
L0641: 1, L0768: 1,
L0649: 1, L0514: 1,
L0659: 1, L0783: 1,
L0788: 1, L0664: 1,
L0665: 1, L0438: 1,
H0547: 1, H0435: 1,
H0522: 1, H0696: 1,
S0404: 1, H0478: 1,
L0742: 1, L0740: 1,
L0749: 1, L0758: 1,
S0434: 1, S0194: 1, |
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|-----|---------|--------|-----|-----------|-----|--|--|--|--|
| 106 | HISDS62 | 935932 | 116 | 1 - 519 | 729 | Ser-11 to Trp-16,
Ile-20 to Trp-26,
Asn-37 to Ser-58,
Leu-67 to Gln-72,
Lys-101 to Asp-108,
Asp-135 to Tyr-140. | H0422: 1 and H0506: 1.
AR089: 2, AR061: 1
T0049: 1, S0278: 1,
H0031: 1 and H0539: 1. | | |
| 107 | HLQDT35 | 839777 | 117 | 222 - 494 | 730 | | AR089: 3, AR061: 3
S0358: 8, L0766: 7,
L0777: 7, L0731: 7,
L0659: 4, L0748: 4,
L0751: 4, L0783: 3,
L0663: 3, S0418: 2,
S0360: 2, H0486: 2,
S0010: 2, S0250: 2,
S0422: 2, L0763: 2,
L0803: 2, L0775: 2,
L0789: 2, H0520: 2,
L0756: 2, L0752: 2,
H0656: 1, S0376: 1,
H0208: 1, H0574: 1,
H0632: 1, S0414: 1,
H0581: 1, H0052: 1,
H0024: 1, H0014: 1,
H0355: 1, H0688: 1,
H0090: 1, H0623: 1, | | |

FORM NO. 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 118, 119, 120, 121, 122, 123, 124, 125, 126, 127, 128, 129, 130, 131, 132, 133, 134, 135, 136, 137, 138, 139, 140, 141, 142, 143, 144, 145, 146, 147, 148, 149, 150, 151, 152, 153, 154, 155, 156, 157, 158, 159, 160, 161, 162, 163, 164, 165, 166, 167, 168, 169, 170, 171, 172, 173, 174, 175, 176, 177, 178, 179, 180, 181, 182, 183, 184, 185, 186, 187, 188, 189, 190, 191, 192, 193, 194, 195, 196, 197, 198, 199, 200, 201, 202, 203, 204, 205, 206, 207, 208, 209, 210, 211, 212, 213, 214, 215, 216, 217, 218, 219, 220, 221, 222, 223, 224, 225, 226, 227, 228, 229, 230, 231, 232, 233, 234, 235, 236, 237, 238, 239, 240, 241, 242, 243, 244, 245, 246, 247, 248, 249, 250, 251, 252, 253, 254, 255, 256, 257, 258, 259, 260, 261, 262, 263, 264, 265, 266, 267, 268, 269, 270, 271, 272, 273, 274, 275, 276, 277, 278, 279, 280, 281, 282, 283, 284, 285, 286, 287, 288, 289, 290, 291, 292, 293, 294, 295, 296, 297, 298, 299, 300, 301, 302, 303, 304, 305, 306, 307, 308, 309, 310, 311, 312, 313, 314, 315, 316, 317, 318, 319, 320, 321, 322, 323, 324, 325, 326, 327, 328, 329, 330, 331, 332, 333, 334, 335, 336, 337, 338, 339, 340, 341, 342, 343, 344, 345, 346, 347, 348, 349, 350, 351, 352, 353, 354, 355, 356, 357, 358, 359, 360, 361, 362, 363, 364, 365, 366, 367, 368, 369, 370, 371, 372, 373, 374, 375, 376, 377, 378, 379, 380, 381, 382, 383, 384, 385, 386, 387, 388, 389, 390, 391, 392, 393, 394, 395, 396, 397, 398, 399, 400, 401, 402, 403, 404, 405, 406, 407, 408, 409, 410, 411, 412, 413, 414, 415, 416, 417, 418, 419, 420, 421, 422, 423, 424, 425, 426, 427, 428, 429, 430, 431, 432, 433, 434, 435, 436, 437, 438, 439, 440, 441, 442, 443, 444, 445, 446, 447, 448, 449, 450, 451, 452, 453, 454, 455, 456, 457, 458, 459, 460, 461, 462, 463, 464, 465, 466, 467, 468, 469, 470, 471, 472, 473, 474, 475, 476, 477, 478, 479, 480, 481, 482, 483, 484, 485, 486, 487, 488, 489, 490, 491, 492, 493, 494, 495, 496, 497, 498, 499, 500, 501, 502, 503, 504, 505, 506, 507, 508, 509, 510, 511, 512, 513, 514, 515, 516, 517, 518, 519, 520, 521, 522, 523, 524, 525, 526, 527, 528, 529, 530, 531, 532, 533, 534, 535, 536, 537, 538, 539, 540, 541, 542, 543, 544, 545, 546, 547, 548, 549, 550, 551, 552, 553, 554, 555, 556, 557, 558, 559, 560, 561, 562, 563, 564, 565, 566, 567, 568, 569, 570, 571, 572, 573, 574, 575, 576, 577, 578, 579, 580, 581, 582, 583, 584, 585, 586, 587, 588, 589, 590, 591, 592, 593, 594, 595, 596, 597, 598, 599, 600, 601, 602, 603, 604, 605, 606, 607, 608, 609, 610, 611, 612, 613, 614, 615, 616, 617, 618, 619, 620, 621, 622, 623, 624, 625, 626, 627, 628, 629, 630, 631, 632, 633, 634, 635, 636, 637, 638, 639, 640, 641, 642, 643, 644, 645, 646, 647, 648, 649, 650, 651, 652, 653, 654, 655, 656, 657, 658, 659, 660, 661, 662, 663, 664, 665, 666, 667, 668, 669, 670, 671, 672, 673, 674, 675, 676, 677, 678, 679, 680, 681, 682, 683, 684, 685, 686, 687, 688, 689, 690, 691, 692, 693, 694, 695, 696, 697, 698, 699, 700, 701, 702, 703, 704, 705, 706, 707, 708, 709, 710, 711, 712, 713, 714, 715, 716, 717, 718, 719, 720, 721, 722, 723, 724, 725, 726, 727, 728, 729, 730, 731, 732, 733, 734, 735, 736, 737, 738, 739, 740, 741, 742, 743, 744, 745, 746, 747, 748, 749, 750, 751, 752, 753, 754, 755, 756, 757, 758, 759, 760, 761, 762, 763, 764, 765, 766, 767, 768, 769, 770, 771, 772, 773, 774, 775, 776, 777, 778, 779, 780, 781, 782, 783, 784, 785, 786, 787, 788, 789, 790, 791, 792, 793, 794, 795, 796, 797, 798, 799, 800, 801, 802, 803, 804, 805, 806, 807, 808, 809, 810, 811, 812, 813, 814, 815, 816, 817, 818, 819, 820, 821, 822, 823, 824, 825, 826, 827, 828, 829, 830, 831, 832, 833, 834, 835, 836, 837, 838, 839, 840, 841, 842, 843, 844, 845, 846, 847, 848, 849, 850, 851, 852, 853, 854, 855, 856, 857, 858, 859, 860, 861, 862, 863, 864, 865, 866, 867, 868, 869, 870, 871, 872, 873, 874, 875, 876, 877, 878, 879, 880, 881, 882, 883, 884, 885, 886, 887, 888, 889, 890, 891, 892, 893, 894, 895, 896, 897, 898, 899, 900, 901, 902, 903, 904, 905, 906, 907, 908, 909, 910, 911, 912, 913, 914, 915, 916, 917, 918, 919, 920, 921, 922, 923, 924, 925, 926, 927, 928, 929, 930, 931, 932, 933, 934, 935, 936, 937, 938, 939, 940, 941, 942, 943, 944, 945, 946, 947, 948, 949, 950, 951, 952, 953, 954, 955, 956, 957, 958, 959, 960, 961, 962, 963, 964, 965, 966, 967, 968, 969, 970, 971, 972, 973, 974, 975, 976, 977, 978, 979, 980, 981, 982, 983, 984, 985, 986, 987, 988, 989, 990, 991, 992, 993, 994, 995, 996, 997, 998, 999, 1000

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| 108 | HLWFN63 | 908437 | 118 | 404 - 2566 | 731 | Thr-7 to Phe-29,
Thr-37 to Lys-52,
Glu-89 to Val-112. | AR051: 11, AR050: 9,
AR054: 5, AR089: 0,
AR061: 0
H0031: 5, S0222: 4,
S0028: 4, H0662: 3,
L0748: 3, S0260: 3,
S0276: 3, S0282: 2,
S0360: 2, S0046: 2,
H0575: 2, H0196: 2,
S0036: 2, H0268: 2,
L0662: 2, S0027: 2,
L0754: 2, L0747: 2,
L0749: 2, L0756: 2,
L0777: 2, L0604: 2,
L0595: 2, H0171: 1,
S0030: 1, S0029: 1, | H0509: 1, H0529: 1,
L0520: 1, L0761: 1,
L0650: 1, L0809: 1,
L0666: 1, L0665: 1,
S0126: 1, H0684: 1,
H0648: 1, S0390: 1,
L0740: 1, L0745: 1,
L0749: 1, L0750: 1,
L0755: 1, L0591: 1,
L0362: 1 and S0242: 1. | | |
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|-----|---------|--------|-----|-----------|-----|--|--|--|---|--|--|--|--|
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S0300: 1, L0717: 1,
H0550: 1, H0441: 1,
H0431: 1, H0392: 1,
T0060: 1, S0010: 1,
H0052: 1, H0309: 1,
S6028: 1, S0250: 1,
H0252: 1, H0553: 1,
S0364: 1, S0366: 1,
H0433: 1, H0269: 1,
H0412: 1, L0372: 1,
L0804: 1, L0789: 1,
L0666: 1, L0663: 1,
S0126: 1, S0044: 1,
H0345: 1, S0390: 1,
S0037: 1, S3014: 1,
L0743: 1, L0439: 1,
L0750: 1, L0779: 1,
L0599: 1, L0593: 1,
L0366: 1 and H0653: 1. | | | | |
| 109 | HMEFT66 | 856149 | 119 | 2 - 349 | 732 | | | | AR061: 1, AR089: 1
H0175: 1, H0266: 1,
H0292: 1, H0628: 1 and
L0779: 1. | | | | |
| 110 | HMSCD15 | 918133 | 120 | 237 - 635 | 733 | | | | AR089: 1, AR061: 1
S0002: 2 and L0766: 1. | | | | |

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|-----|---------|--------|-----|-----------|-----|--|--|--|--|
| 111 | HMSHO64 | 746582 | 121 | 1 - 411 | 734 | Ser-11 to Ser-21,
Ser-84 to Ala-89,
Pro-98 to Arg-107. | AR089: 2, AR061: 2
S0002: 2 | | |
| 112 | HMTAW83 | 911385 | 122 | 1 - 363 | 735 | Ile-26 to Trp-33,
Glu-52 to Leu-71. | AR089: 0, AR061: 0
H0583: 1, H0644: 1,
L0766: 1 and H0518: 1. | | |
| 113 | HMVAM09 | 963814 | 123 | 2 - 802 | 736 | | AR089: 4, AR061: 1
L0731: 7, L0517: 5,
S0212: 3, L0775: 3,
L0740: 3, H0266: 2,
L0809: 2, H0696: 2,
L0748: 2, S0132: 1,
H0574: 1, H0013: 1,
H0544: 1, H0023: 1,
H0071: 1, H0286: 1,
H0100: 1, H0494: 1,
S0370: 1, L0770: 1,
L0646: 1, L0764: 1,
L0771: 1, L0363: 1,
L0774: 1, L0659: 1,
L0789: 1, L0666: 1,
S0126: 1, H0522: 1,
L0754: 1, L0747: 1 and
L0755: 1. | | |
| 114 | HNSAA28 | 946988 | 124 | 85 - 1557 | 737 | Glu-9 to Ser-20,
Ile-23 to Gly-29, | AR050: 8, AR054: 6,
AR051: 3, AR089: 1, | | |

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|-----|---------|---------|-----|----------|------|------------------|--|---|--|--|
| 116 | HOUDH19 | 935465 | 517 | 1 - 150 | 1130 | Glu-1 to Thr-13. | Gln-291 to Trp-296,
Asn-311 to Phe-321,
Ser-327 to Glu-335,
Lys-364 to Trp-369,
Ala-376 to Gly-384,
Asn-437 to Trp-444,
Met-462 to Trp-472,
Gln-483 to Gly-491,
Thr-499 to Trp-504,
Arg-512 to Ala-517. | L0749: 2, S0134: 1,
H0645: 1, H0587: 1,
H0635: 1, H0581: 1,
H0546: 1, H0477: 1,
H0560: 1, H0641: 1,
S0422: 1, H0529: 1,
L0521: 1, L0662: 1,
L0794: 1, L0774: 1,
L0775: 1, L0606: 1,
L0659: 1, L0647: 1,
L0789: 1, L0791: 1,
L0792: 1, L0666: 1,
L0663: 1, L0665: 1,
H0702: 1, H0547: 1,
H0576: 1, S0028: 1,
L0756: 1, L0777: 1,
L0755: 1, L0758: 1,
H0543: 1 and H0506: 1. | | |
| | | 1150918 | 126 | 506 - 3 | 739 | Pro-8 to Ser-13. | | AR089: 1, AR061: 0
S0040: 1, H0250: 1,
T0048: 1, L0761: 1,
L0764: 1, L0783: 1,
L0809: 1, L0789: 1 and
L0757: 1. | | |
| | | 908588 | 518 | 52 - 573 | 1131 | Thr-8 to Gln-19 | | | | |

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|-----|---------|---------|-----|-----------|------|--|---|--|--|--|--|--|
| | | | | | | | | | L0763: 1, L0772: 1,
L0764: 1, L0771: 1,
L0773: 1, L0650: 1,
L0806: 1, L0659: 1,
L0547: 1, L0809: 1,
L0666: 1, L0663: 1,
L0665: 1, S0328: 1,
S0380: 1, S0390: 1,
S0032: 1, L0744: 1,
L0745: 1, L0746: 1,
L0747: 1, L0756: 1,
L0777: 1, L0758: 1,
L0588: 1, S0276: 1,
S0196: 1, S0412: 1 and
H0506: 1. | | | |
| 122 | HSFAM09 | 1150965 | 132 | 2 - 325 | 745 | Leu-2 to Gly-8. | AR061: 5, AR089: 2
H0154: 2 | | | | | |
| | | 573345 | 519 | 147 - 332 | 1132 | Arg-1 to Ser-8,
Lys-42 to Lys-48. | | | | | | |
| 123 | HSSAX53 | 507509 | 133 | 209 - 361 | 746 | | H0135: 1 and H0063:
1. | | | | | |
| 124 | HSVAW49 | 1150960 | 134 | 220 - 486 | 747 | Pro-19 to Thr-24,
Thr-78 to Lys-89. | AR061: 9, AR089: 7
H0309: 1 | | | | | |
| | | 689674 | 520 | 44 - 208 | 1133 | Glu-21 to Glu-27. | | | | | | |
| 125 | HTEAG49 | 954614 | 135 | 510 - 208 | 748 | | AR089: 1, AR061: 0
L0759: 4, L0770: 2, | | | | | |

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|-----|---------|--------|-----|-----------|-----|---|--|--|---|--|--|--|
| | | | | | | | | | L0794: 4, H0039: 2, S0358: 1, H0013: 1, H0575: 1, L0770: 1, L0769: 1 and L0749: 1. | | | |
| 129 | HTTKP07 | 911390 | 139 | 2 - 337 | 752 | Thr-15 to Asp-25, Glu-69 to Leu-89. | | | AR089: 1, AR061: 1 H0634: 2 | | | |
| 130 | HUCOW17 | 933357 | 140 | 155 - 856 | 753 | Gln-27 to Trp-45. | | | AR089: 4, AR061: 2 L0439: 5, S0002: 3, L0604: 3, H0619: 2, H0024: 2, H0625: 2, L0768: 2, L0757: 2, H0638: 1, S0420: 1, S0360: 1, H0586: 1, L0163: 1, S0214: 1, L0143: 1, H0264: 1, L0769: 1, L0764: 1, L0774: 1, L0651: 1, L0659: 1, L0542: 1, L0789: 1, H0539: 1, H0521: 1, S0044: 1, L0777: 1, L0758: 1, L0599: 1 and H0422: 1. | | | |
| 131 | HWHGF52 | 726102 | 141 | 1 - 453 | 754 | Gln-1 to Lys-8, Gly-10 to Trp-17, Val-28 to Gly-43, Thr-54 to Glu-63. | | | AR089: 1, AR061: 0 L0776: 5, L0764: 4, L0743: 4, L0740: 3, L0750: 3, L0777: 3, | | | |

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| 133 | HWLFBH94 | 690442 | 521 | 1 - 261 | 1134 | Gly-1 to Ser-7. | AR089: 5, AR061: 2
S0358: 5, L0596: 3,
L0771: 2, L0758: 2,
S0354: 1, S0376: 1,
T0109: 1, H0036: 1,
H0590: 1, L0040: 1,
H0038: 1, H0616: 1,
L0646: 1, L0764: 1,
L0768: 1, L0775: 1,
L0659: 1 and S0404: 1. | | |
| | | 909682 | 522 | 134 - 535 | 1135 | Ser-25 to Ala-52,
Phe-64 to Glu-71. | | | |
| 134 | HWMBM13 | 909683 | 144 | 3 - 539 | 757 | Pro-11 to Ala-35,
Phe-47 to Glu-54,
Glu-78 to Gly-83,
Gln-94 to Ser-106,
Ser-114 to Val-120. | AR089: 2, AR061: 2
S0358: 6, L0794: 4,
L0758: 4, S0354: 3,
L0779: 3, L0596: 3,
S0376: 2, H0036: 2,
H0620: 2, H0063: 2,
L0771: 2, L0803: 2,
L0654: 2, L0659: 2,
T0109: 1, H0013: 1,
H0590: 1, H0052: 1,
H0596: 1, T0110: 1,
L0040: 1, H0090: 1,
H0038: 1, H0040: 1, | | |

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| 138 | HFKLA09 | | | | | | Gly-30 to Gly-35,
Ser-50 to Glu-61,
Ala-74 to Pro-81. | H0254: 2, H0255: 2,
S0045: 2, H0266: 2,
H0052: 1, H0050: 1,
H0063: 1, H0488: 1 and
H0423: 1. | | |
| | | 911262 | 524 | 1 - 597 | 1137 | | Pro-9 to Lys-25,
Gly-36 to Gly-41,
Ser-56 to Glu-67,
Ala-80 to Pro-87. | | | |
| 138 | HFKLA09 | 117800 | 148 | 3 - 1574 | 761 | | His-1 to Asp-11,
Val-33 to Pro-57,
Gly-68 to Glu-74,
Pro-76 to Pro-81,
Phe-93 to Val-120,
Pro-131 to Pro-146,
Pro-161 to Pro-168,
Tyr-178 to Ser-184,
Pro-187 to Gly-215,
Asn-229 to Asn-244,
Asp-250 to Trp-255,
Pro-258 to Asp-263,
Pro-300 to Val-310,
Asp-364 to Glu-371,
Thr-441 to Lys-446,
Ser-462 to Thr-477,
Lys-487 to Trp-492. | AR061: 4, AR089: 2
L0777: 11, L0748: 10,
L0803: 8, L0794: 7,
L0750: 6, H0620: 5,
L0749: 5, H0622: 4,
L0805: 4, L0809: 4,
L0665: 4, H0550: 3,
H0575: 3, H0023: 3,
L0659: 3, L0790: 3,
S0356: 2, H0549: 2,
S0222: 2, H0592: 2,
H0427: 2, L0157: 2,
H0213: 2, L0763: 2,
L0662: 2, L0774: 2,
L0789: 2, L0666: 2,
H0539: 2, L0743: 2,
L0744: 2, L0600: 2, | | |
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| | | | | | S0282: 1, H0664: 1,
L0005: 1, S0358: 1,
S0360: 1, H0411: 1,
H0441: 1, H0587: 1,
S0280: 1, H0156: 1,
H0618: 1, H0309: 1,
H0327: 1, H0545: 1,
H0050: 1, H0012: 1,
H0051: 1, S0051: 1,
H0375: 1, H0687: 1,
H0292: 1, H0424: 1,
H0553: 1, H0617: 1,
H0124: 1, S0366: 1,
H0616: 1, H0100: 1,
S0210: 1, L0536: 1,
L0769: 1, L0637: 1,
L0644: 1, L0764: 1,
L0804: 1, L0650: 1,
L0784: 1, L0655: 1,
L0367: 1, L0368: 1,
L0663: 1, S0126: 1,
S0330: 1, S0044: 1,
L0740: 1, L0747: 1,
L0752: 1, L0758: 1,
L0759: 1, S0194: 1 and
H0352: 1. |
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| | L0768: 3, L0666: 3,
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L0477: 1, T0039: 1,
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H0023: 1, H0051: 1,
T0079: 1, H0355: 1,
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S0250: 1, H0628: 1, | |
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| 143 | HTLIT05 | 1217625 | 153 | 81 - 623 | 766 | | | L0599: 1, L0608: 1,
L0594: 1, L0603: 1,
H0668: 1, H0665: 1,
H0667: 1, S0194: 1,
H0542: 1, H0423: 1,
H0422: 1, S0424: 1 and
H0506: 1. | | |
| 144 | HAPNV33 | | | | | | | AR054: 41, AR050:
39, AR051: 30, AR089:
7, AR061: 5
H0618: 2, H0040: 1
and H0522: 1. | | |
| | | 1095161 | 528 | 149 - 622 | 1141 | | Thr-27 to Asn-33,
Thr-63 to Asp-69. | | | |
| | | 1151374 | 154 | 1 - 774 | 767 | | Gln-93 to Arg-105,
Ser-130 to Ile-135,
Ser-166 to Lys-175,
Ser-238 to Glu-243. | AR061: 7, AR089: 2
H0619: 1, H0575: 1,
H0615: 1 and S0028: 1. | | |
| 145 | HBTAE84 | 947872 | 529 | 1 - 477 | 1142 | | Gln-93 to Arg-105,
Ser-130 to Ile-135. | | | |
| | | 1128800 | 155 | 3 - 416 | 768 | | Thr-45 to Phe-55,
Leu-62 to Asn-67. | AR089: 1, AR061: 0
S0180: 1 | | |
| 146 | HDPVY89 | 781946 | 530 | 2 - 295 | 1143 | | Thr-41 to Phe-51,
Leu-58 to Asn-63. | | | |
| | | 827026 | 156 | 2 - 580 | 769 | | Ile-8 to Arg-16,
Leu-104 to Asp-110, | AR089: 4, AR061: 3
H0657: 3, H0253: 3, | | |

| | | | | | | | | | |
|-----|---------|---------|-----|--------------------|-------------|--|---|--|--|
| 147 | HGLDB21 | 1010920 | 157 | 240 - 1388 | 770 | Leu-20 to Pro-34,
Lys-36 to Leu-55,
Arg-63 to Gln-72,
Pro-215 to Thr-222,
Ile-288 to Leu-297,
Ala-337 to Gly-346. | S0424: 1, H0506: 1 and
H0008: 1.
AR061: 10, AR089: 4
H0688: 2, L0803: 2,
L0666: 2, L0749: 2,
L0777: 2, L0594: 2,
S0218: 1, H0657: 1,
H0656: 1, H0341: 1,
H0663: 1, H0351: 1,
H0370: 1, H0318: 1,
T0103: 1, H0024: 1,
H0652: 1, L0769: 1,
L0800: 1, L0794: 1,
L0766: 1, L0561: 1,
L0804: 1, L0657: 1,
L0636: 1, L0635: 1,
L0789: 1, L0663: 1,
L0665: 1, L0750: 1 and
H0216: 1. | | |
| 148 | HMIAN37 | 947881 | 158 | 3 - 230
1 - 645 | 1144
771 | Ala-30 to Gly-39.
Asp-60 to Lys-75,
Glu-136 to Gln-142. | AR061: 2, AR089: 1
S0414: 26, L0439: 12,
L0766: 10, L0779: 10,
L0777: 10, L0758: 10,
L0757: 8, L0752: 7,
L0740: 5, H0170: 4, | | |

L0717: 1, H0550: 1,
H0600: 1, H0333: 1,
H0574: 1, L0622: 1,
T0114: 1, H0427: 1,
H0599: 1, H0575: 1,
T0082: 1, H0036: 1,
S0346: 1, H0318: 1,
S0474: 1, S0049: 1,
H0178: 1, H0050: 1,
H0012: 1, H0620: 1,
S0050: 1, S0362: 1,
L0163: 1, T0010: 1,
H0510: 1, S6028: 1,
S0250: 1, H0252: 1,
H0615: 1, H0428: 1,
H0031: 1, H0181: 1,
L0055: 1, H0124: 1,
S0036: 1, H0623: 1,
H0494: 1, H0633: 1,
L0763: 1, L0770: 1,
L0768: 1, L0766: 1,
L0375: 1, L0651: 1,
L0378: 1, L0653: 1,
L0606: 1, L0783: 1,
L0790: 1, L0663: 1,
L0665: 1, H0144: 1,

| Year | 1977 | 1978 | 1979 | 1980 | 1981 | 1982 | 1983 | 1984 | 1985 | 1986 | 1987 | 1988 | 1989 | 1990 | 1991 | 1992 | 1993 | 1994 | 1995 | 1996 | 1997 | 1998 | 1999 | 2000 | 2001 | 2002 | 2003 | 2004 | 2005 | 2006 | 2007 | 2008 | 2009 | 2010 | 2011 | 2012 | 2013 | 2014 | 2015 | 2016 | 2017 | 2018 | 2019 | 2020 | 2021 | 2022 | 2023 | 2024 | 2025 | 2026 | 2027 | 2028 | 2029 | 2030 | 2031 | 2032 | 2033 | 2034 | 2035 | 2036 | 2037 | 2038 | 2039 | 2040 | 2041 | 2042 | 2043 | 2044 | 2045 | 2046 | 2047 | 2048 | 2049 | 2050 | 2051 | 2052 | 2053 | 2054 | 2055 | 2056 | 2057 | 2058 | 2059 | 2060 | 2061 | 2062 | 2063 | 2064 | 2065 | 2066 | 2067 | 2068 | 2069 | 2070 | 2071 | 2072 | 2073 | 2074 | 2075 | 2076 | 2077 | 2078 | 2079 | 2080 | 2081 | 2082 | 2083 | 2084 | 2085 | 2086 | 2087 | 2088 | 2089 | 2090 | 2091 | 2092 | 2093 | 2094 | 2095 | 2096 | 2097 | 2098 | 2099 | 2100 |
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| 1977 | 1978 | 1979 | 1980 | 1981 | 1982 | 1983 | 1984 | 1985 | 1986 | 1987 | 1988 | 1989 | 1990 | 1991 | 1992 | 1993 | 1994 | 1995 | 1996 | 1997 | 1998 | 1999 | 2000 | 2001 | 2002 | 2003 | 2004 | 2005 | 2006 | 2007 | 2008 | 2009 | 2010 | 2011 | 2012 | 2013 | 2014 | 2015 | 2016 | 2017 | 2018 | 2019 | 2020 | 2021 | 2022 | 2023 | 2024 | 2025 | 2026 | 2027 | 2028 | 2029 | 2030 | 2031 | 2032 | 2033 | 2034 | 2035 | 2036 | 2037 | 2038 | 2039 | 2040 | 2041 | 2042 | 2043 | 2044 | 2045 | 2046 | 2047 | 2048 | 2049 | 2050 | 2051 | 2052 | 2053 | 2054 | 2055 | 2056 | 2057 | 2058 | 2059 | 2060 | 2061 | 2062 | 2063 | 2064 | 2065 | 2066 | 2067 | 2068 | 2069 | 2070 | 2071 | 2072 | 2073 | 2074 | 2075 | 2076 | 2077 | 2078 | 2079 | 2080 | 2081 | 2082 | 2083 | 2084 | 2085 | 2086 | 2087 | 2088 | 2089 | 2090 | 2091 | 2092 | 2093 | 2094 | 2095 | 2096 | 2097 | 2098 | 2099 | 2100 | |

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| | | | | | | | | | L0803: 1, L0651: 1,
L0791: 1, H0539: 1,
H0521: 1, L0780: 1,
L0753: 1, L0758: 1 and
S0192: 1. | | |
| | 949211 | 537 | 185 - 778 | 1150 | Tyr-7 to Tyr-15,
Pro-43 to Ala-52,
Gln-57 to Ala-62,
Asn-68 to Ala-73,
Tyr-75 to Met-83,
Glu-115 to Leu-140,
Ala-144 to Glu-156,
Val-159 to Ser-166,
Arg-178 to Pro-186,
Arg-191 to Ile-198. | | | | AR089: 4, AR061: 2
H0551: 2, H0581: 1,
H0560: 1, H0414: 1,
S0152: 1 and H0522: 1. | | |
| 155 | HAMGX15 | 1177932 | 165 | 293 - 763 | 778 | | | | | | |
| | 908840 | 538 | 428 - 757 | 1151 | Ala-54 to Ile-59,
His-71 to His-82. | | | | | | |
| 156 | HAUBV06 | 1106041 | 166 | 1164 - 2108 | 779 | Met-5 to Asn-11,
Gly-20 to Arg-30,
Thr-36 to Ile-41,
His-136 to Thr-143,
Thr-152 to Asp-161, | | | AR061: 1, AR089: 0
S0052: 2, S0028: 2,
H0624: 1, H0294: 1,
S0001: 1, S0282: 1,
H0250: 1, H0271: 1, | | |

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| | | | | | | | Gly-176 to Cys-183. | H0189: 1, S0150: 1,
S0428: 1, S0031: 1 and
S0260: 1. | | |
| | 596802 | 539 | 3 - 1025 | 1152 | | | Arg-1 to Lys-11,
Thr-23 to Arg-28,
Gly-70 to Ala-76,
Lys-118 to Thr-125,
Pro-161 to His-168,
Arg-170 to Lys-175,
Glu-222 to Leu-228,
Pro-259 to Gly-265,
Asn-299 to Leu-305,
Leu-309 to Gly-314,
Pro-316 to Ser-327. | | | |
| | 929762 | 540 | 2211 - 1192 | 1153 | | | Asn-1 to Lys-10,
Thr-22 to Arg-27,
Gly-69 to Ala-75. | | | |
| 157 | HBWCM62 | 167 | 1 - 477 | 780 | | | Glu-7 to Tyr-14,
Arg-21 to Leu-29,
Pro-42 to Ala-54,
Arg-95 to Phe-106. | AR089: 2, AR061: 1
H0341: 2, H0052: 2,
H0556: 1, H0656: 1,
S0354: 1, H0427: 1,
H0040: 1, H0488: 1,
H0059: 1 and S0386: 1. | | |
| | 908818 | 541 | 1 - 477 | 1154 | | | Glu-7 to Tyr-14,
Arg-21 to Lys-30. | | | |
| 158 | HCWFA35 | 168 | 237 - 623 | 781 | | | Asn-54 to Asn-63, | AR089: 13, AR061: 6 | | |

| | | | | | | | | | |
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| 162 | HEOPR74 | 935730
1226822 | 545
172 | 161 - 445
2 - 937 | 1158
785 | Gln-38 to Ser-51.
Pro-1 to Gln-8,
Lys-32 to Lys-45,
Pro-51 to Arg-59,
Asp-84 to Val-107,
Ala-113 to Leu-135,
Gln-137 to Leu-156,
Gln-160 to Arg-170,
Gln-182 to Pro-194,
Lys-201 to Ser-213,
Arg-272 to Tyr-278. | AR089: 3, AR061: 2
H0457: 8, H0264: 2,
H0645: 1, H0549: 1,
H0069: 1, H0599: 1,
H0318: 1, H0566: 1,
H0132: 1, H0658: 1 and
S0350: 1. | | |
| | | 908836 | 546 | 2 - 649 | 1159 | Pro-1 to Gln-8,
Lys-32 to Lys-45,
Pro-51 to Arg-59,
Asp-84 to Val-107,
Ala-113 to Leu-135,
Gln-137 to Leu-156,
Gln-160 to Arg-170,
Gln-182 to Leu-198. | | | |
| 163 | HIBEK35 | 731480 | 173 | 3 - 416 | 786 | | AR089: 0, AR061: 0
T0010: 2 | | |
| 164 | HJMAR88 | 1104937 | 174 | 3 - 551 | 787 | Ala-11 to Asn-16,
Ala-18 to Leu-25,
Lys-40 to Arg-52,
Tyr-58 to Ile-76,
Lys-151 to Thr-162, | AR089: 14, AR061: 5
H0545: 1, H0560: 1
and L0805: 1. | | |

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|-----|---------|---------|-----|----------|-----|---|--|--|--|
| 166 | HOUDS09 | 1164010 | 176 | 3 - 1121 | 789 | Asn-178 to Gln-194,
Arg-197 to His-202,
Ser-236 to Arg-241,
Gln-245 to Arg-250.
Ala-15 to Gln-22,
Pro-55 to Val-91,
Glu-116 to Tyr-122,
His-130 to His-135,
Asn-155 to Tyr-162,
Leu-164 to Cys-186,
Ser-213 to Gln-222,
Ser-228 to Gly-239,
Ile-281 to Glu-286,
Lys-296 to Lys-303,
Val-310 to Glu-315,
Thr-320 to Asp-335,
Arg-344 to Ala-352. | AR061: 153, AR089:
48
L0599: 12, L0766: 11,
L0754: 8, L0803: 2,
L0809: 2, L0743: 2,
L0731: 2, H0624: 1,
H0171: 1, S0040: 1,
H0650: 1, H0656: 1,
S0298: 1, S0282: 1,
H0580: 1, S0046: 1,
S0222: 1, H0431: 1,
H0587: 1, H0486: 1,
S0010: 1, H0318: 1,
H0581: 1, H0309: 1,
H0416: 1, T0006: 1,
H0063: 1, T0041: 1,
H0560: 1, S0422: 1,
S0002: 1, L0641: 1,
L0363: 1, L0523: 1,
L0659: 1, H0547: 1,
H0539: 1, S0152: 1,
H0521: 1, L0758: 1, | | |
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| | | | | | | | | | | S0242: 1, H0543: 1 and
H0423: 1. | | |
| | | 949051 | 549 | 16 - 906 | 1162 | Cys-3 to Glu-8,
Gly-13 to Gln-19,
Pro-52 to Val-88. | | | | | | |
| 167 | HTEGM38 | 675087 | 177 | 84 - 263 | 790 | Ala-15 to Tyr-24,
His-32 to Asp-39. | | | | AR089: 1, AR061: 0
H0038: 2 | 11q25 | 602782 |
| 168 | HTEKY82 | 1152495 | 178 | 499 - 125 | 791 | Gln-85 to Gly-91,
Ser-99 to Arg-104. | | | | AR061: 5, AR089: 2
H0038: 3, H0575: 1,
H0052: 1, H0628: 1,
H0412: 1, L0780: 1 and
L0758: 1. | | |
| | | 908846 | 550 | 122 - 517 | 1163 | | | | | | | |
| 169 | HTLCY54 | 1193550 | 179 | 1043 - 510 | 792 | | | | | AR061: 5, AR089: 5
H0253: 4, H0618: 3,
L0758: 3, L0779: 2 and
L0794: 1. | | |
| | | 908832 | 551 | 134 - 934 | 1164 | Arg-1 to Arg-6,
Ala-49 to Tyr-58,
Pro-67 to Lys-80,
Ser-92 to Trp-108. | | | | | | |
| 170 | HFOXK14 | 603245 | 180 | 150 - 401 | 793 | Ala-6 to Tyr-17. | | | | AR089: 19, AR061: 8
L0747: 5, L0731: 2,
H0656: 1, H0351: 1,
H0392: 1, H0333: 1,
S0362: 1, S0306: 1, | | |

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|-----|---------|--------|-----|---------|-----|---|--|---|--|--|
| 176 | HAHY08 | 962113 | 186 | 3 - 278 | 799 | | | H0131: 1, H0130: 1,
H0646: 1, S0144: 1,
S0426: 1, H0529: 1,
L0565: 1, H0547: 1,
H0689: 1, H0435: 1,
H0670: 1, S0330: 1,
H0521: 1, S0027: 1,
S0028: 1, S0032: 1,
L0439: 1, L0747: 1,
L0759: 1, S0260: 1,
H0445: 1, L0597: 1,
L0604: 1, L0593: 1,
L0366: 1, H0668: 1,
S0242: 1 and H0422: 1. | | |
| 177 | HBIOZ10 | 973131 | 187 | 3 - 503 | 800 | Leu-50 to Asp-61,
Ser-100 to Leu-107,
Ala-120 to Thr-130. | AR054: 189, AR051:
68, AR050: 35, AR089:
4, AR061: 3
H0593: 1 | AR061: 10, AR089: 6 | | |
| 178 | HBKDI30 | 729048 | 188 | 1 - 381 | 801 | Gly-15 to Thr-21,
Glu-76 to Lys-86. | AR089: 1, AR061: 0
S0364: 3, S0366: 3,
L0604: 3, H0624: 1,
L0622: 1, L0623: 1,
H0041: 1, L0791: 1,
S0380: 1 and L0748: 1. | | | |

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| 179 | HBXBW40 | 706115 | 189 | 124 - 456 | 802 | Gln-3 to Ser-12,
Arg-33 to Arg-50,
Ser-93 to Glu-98. | AR089: 16, AR061: 8
S0038: 2, H0438: 1,
S0049: 1 and H0547: 1. | | |
| 180 | HCEHE35 | 909937 | 190 | 3 - 392 | 803 | Asn-6 to Pro-13. | AR061: 8, AR089: 3
S0222: 1, H0052: 1,
H0194: 1, H0290: 1 and
H0264: 1. | | |
| 181 | HCEPW85 | 911374 | 191 | 3 - 314 | 804 | Thr-2 to Gln-7. | H0052: 1 and L0471:
1. | | |
| 182 | HCFAT25 | 932068 | 192 | 82 - 588 | 805 | Lys-15 to Ser-20,
Arg-51 to Arg-60,
Lys-64 to Pro-101. | AR061: 2, AR089: 2
S0358: 1, H0413: 1,
L0502: 1, L0657: 1,
H0522: 1 and H0422: 1. | | |
| 183 | HCFCF47 | 1139731 | 193 | 3 - 764 | 806 | Leu-1 to Glu-9,
Gln-43 to Ala-52,
Gly-169 to Gly-176,
Arg-178 to Leu-185,
Pro-192 to Phe-199. | AR089: 14, AR061: 7
H0341: 1 and H0422:
1. | | |
| | | 894415 | 552 | 2 - 298 | 1165 | Arg-1 to Glu-8. | | | |
| 184 | HDAAV61 | 810305 | 194 | 2 - 343 | 807 | Asp-90 to Lys-105. | AR089: 25, AR061: 11
L0601: 5, H0266: 4,
S0222: 3, H0265: 2,
H0556: 2, H0575: 2,
H0052: 2, H0271: 2,
S0114: 1, S0134: 1,
S0420: 1, H0393: 1, | 109690,
109690,
123101,
180071,
600584 | 5q34 |

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|-----|---------|--------|-----|-----------|-----|---|--|--|--|---|--|--|
| | | | | | | | | | H0550: 1, H0497: 1,
H0318: 1, H0581: 1,
H0251: 1, T0115: 1,
H0014: 1, H0286: 1,
H0494: 1, H0561: 1,
L0766: 1, L0657: 1,
H0698: 1, H0684: 1,
S0330: 1, H0521: 1,
S3014: 1, L0777: 1,
S0260: 1, L0591: 1,
L0594: 1 and H0543: 1. | | | |
| 185 | HDPKD75 | 810824 | 195 | 2 - 445 | 808 | Ala-13 to Asn-20,
Phe-38 to Gly-46,
Gln-89 to His-95. | | | AR089: 4, AR061: 0
H0581: 1, H0494: 1,
H0521: 1, H0543: 1 and
L0465: 1. | | | |
| 186 | HDPNC96 | 934520 | 196 | 3 - 734 | 809 | Val-2 to Gly-8,
Asp-20 to Gln-26. | | | AR089: 1, AR061: 1
H0522: 2 and L0766:
1. | | | |
| 187 | HDPSP15 | 969666 | 197 | 168 - 785 | 810 | Pro-26 to Leu-34,
His-42 to Asn-51. | | | AR061: 2, AR089: 2
L0759: 12, L0439: 11,
L0766: 7, L0775: 5,
H0521: 5, L0755: 5,
L0748: 4, L0756: 4,
L0777: 4, L0731: 4,
L0581: 4, L0619: 3,
L0666: 3, L0779: 3, | 9 | | |

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| L0757: 3, L0588: 3,
S0418: 2, L0618: 2,
H0580: 2, L0055: 2,
L0769: 2, L0773: 2,
L0774: 2, L0791: 2,
L0747: 2, L0750: 2,
H0265: 1, H0663: 1,
S0356: 1, H0208: 1,
H0370: 1, H0108: 1,
H0575: 1, H0618: 1,
H0544: 1, H0545: 1,
S0050: 1, H0510: 1,
H0286: 1, H0031: 1,
H0644: 1, H0068: 1,
H0135: 1, L0564: 1,
H0494: 1, L0475: 1,
H0396: 1, S0144: 1,
S0002: 1, S0426: 1,
L0763: 1, L0761: 1,
L0642: 1, L0764: 1,
L0662: 1, L0768: 1,
L0806: 1, L0661: 1,
L0659: 1, L0367: 1,
L0663: 1, H0519: 1,
H0435: 1, H0658: 1,
S3014: 1, L0751: 1, |
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| | | | | | | | | L0749: 1, L0603: 1,
H0665: 1 and H0542: 1. | | |
| 188 | HDQDX20 | 919027 | 198 | 210 - 1037 | 811 | Met-7 to Ser-12,
Ser-20 to Arg-30,
Asp-85 to Ala-92,
Met-119 to Asn-146,
Pro-151 to Asp-161. | | AR089: 30, AR061: 4
H0521: 3, H0051: 2,
L0756: 2, H0590: 1,
S0250: 1, L0772: 1,
H0522: 1, S0406: 1 and
L0748: 1. | | |
| 189 | HDQHB19 | 1226089 | 199 | 1 - 747 | 812 | Phe-73 to Pro-81,
His-156 to Asp-165,
Pro-182 to Lys-187,
Lys-196 to Asp-201,
Pro-204 to Leu-214,
Pro-224 to Asp-231. | | AR061: 3, AR089: 3
L0759: 12, L0439: 11,
L0766: 7, L0775: 5,
H0521: 5, L0755: 5,
L0748: 4, L0756: 4,
L0777: 4, L0731: 4,
L0581: 4, L0619: 3,
L0666: 3, L0779: 3,
L0757: 3, L0588: 3,
S0418: 2, L0618: 2,
H0580: 2, L0055: 2,
L0769: 2, L0773: 2,
L0774: 2, L0791: 2,
L0747: 2, L0750: 2,
H0265: 1, H0663: 1,
S0356: 1, H0208: 1,
H0370: 1, H0108: 1,
H0575: 1, H0618: 1, | | |

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| 190 | HDTBY88 | 895106 | 553 | 2 - 538 | 1166 | Pro-14 to Ala-20,
Pro-51 to Leu-59,
His-67 to Thr-77. | H0544: 1, H0545: 1,
S0050: 1, H0510: 1,
H0286: 1, H0031: 1,
H0644: 1, H0068: 1,
H0135: 1, L0564: 1,
H0494: 1, L0475: 1,
H0396: 1, S0144: 1,
S0002: 1, S0426: 1,
L0763: 1, L0761: 1,
L0642: 1, L0764: 1,
L0662: 1, L0768: 1,
L0806: 1, L0661: 1,
L0659: 1, L0367: 1,
L0663: 1, H0519: 1,
H0435: 1, H0658: 1,
S3014: 1, L0751: 1,
L0749: 1, L0603: 1,
H0665: 1 and H0542: 1. | | |
| 191 | HE2KZ07 | 934472 | 200 | 3 - 464 | 813 | His-130 to Lys-140. | AR089: 8, AR061: 2
S0218: 1 and H0486: 1. | | |
| | | 909948 | 201 | 2 - 796 | 814 | Leu-10 to Gly-16,
Pro-37 to Glu-45,
Glu-78 to Cys-87. | AR061: 9, AR089: 4
H0624: 1 | | |

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| 192 | HE8UY74 | 960914 | 202 | 111 - 455 | 815 | | AR061: 2, AR089: 1
H0013: 1 and S0027: 1. | | |
| 193 | HE9NO66 | 974353 | 203 | 362 - 871 | 816 | Phe-8 to Lys-27,
Ser-79 to Ser-87,
Cys-102 to Val-116. | AR061: 1, AR089: 1
L0774: 2 and H0144: 2. | | |
| 194 | HEMBT61 | 939957 | 204 | 1 - 351 | 817 | | AR061: 8, AR089: 4
L0547: 2, S0046: 1,
L0471: 1, L0772: 1,
L0529: 1 and L0780: 1. | | |
| 195 | HE1LF29 | 909762 | 205 | 3 - 416 | 818 | | AR061: 4, AR089: 2
H0046: 1 and L0758: 1. | | |
| 196 | HFIUE75 | 909758 | 206 | 2 - 775 | 819 | Cys-1 to Val-10,
Ala-14 to Met-22. | AR089: 1, AR061: 1
L0748: 5, S0242: 3,
H0615: 2, S0376: 1,
S0360: 1, L0717: 1,
L0641: 1, L0766: 1,
L0664: 1, H0478: 1,
L0593: 1 and S0196: 1. | | |
| 197 | HFKIT06 | 934019 | 207 | 1 - 300 | 820 | Asp-2 to Pro-7,
Pro-15 to Gln-20. | AR089: 0, AR061: 0
H0620: 2, L0761: 2,
L0766: 2, L0744: 2,
L0754: 2, L0596: 2,
H0686: 1, H0295: 1,
H0657: 1, H0597: 1,
H0009: 1, H0264: 1, | | |

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| 202 | HKAKM10 | 918685 | 212 | 2 - 547 | 825 | Gly-25 to Gln-31,
Asn-58 to Leu-63,
Lys-71 to His-76,
Ile-82 to Arg-88,
Ala-134 to Thr-139. | AR089: 1, AR061: 1
L0794: 4, L0438: 4,
L0761: 3, L0766: 3,
L0748: 3, L0439: 3,
H0556: 2, L0602: 2,
L0754: 2, L0779: 2,
H0580: 1, H0208: 1,
H0013: 1, T0082: 1,
S0010: 1, H0428: 1,
H0553: 1, H0038: 1,
H0616: 1, H0494: 1, | H0135: 1, H0616: 1,
H0413: 1, H0623: 1,
L0351: 1, S0150: 1,
L0769: 1, L0372: 1,
L0662: 1, L0794: 1,
L0775: 1, L0651: 1,
L0527: 1, L0657: 1,
L0666: 1, H0144: 1,
H0547: 1, H0690: 1,
H0658: 1, H0672: 1,
H0539: 1, S0378: 1,
H0555: 1, L0754: 1,
L0747: 1, L0780: 1,
L0596: 1, S0192: 1,
H0542: 1 and H0423: 1. | | |
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| | | | | | | | | | L0787: 1, H0547: 1,
H0521: 1, H0696: 1,
H0555: 1, L0747: 1,
L0749: 1, L0786: 1,
L0779: 1, L0780: 1,
L0752: 1 and L0592: 1. | | | |
| 207 | HNTMD79 | 934522 | 217 | 182 - 586 | 830 | | | | AR089: 2, AR061: 2
H0519: 2, S0420: 1,
T0114: 1, H0013: 1,
S0346: 1, H0038: 1,
S0142: 1, H0520: 1,
H0521: 1 and H0136: 1. | | | |
| 208 | HNTMH70 | 757184 | 218 | 2 - 688 | 831 | Pro-1 to Glu-6,
His-17 to Lys-22,
Pro-52 to Gln-58. | | | AR089: 0, AR061: 0
H0520: 1 | | | |
| 209 | HNTNB14 | 909942 | 219 | 2 - 658 | 832 | Ala-2 to Gln-9,
Arg-22 to Val-29,
Glu-51 to Leu-64. | | | AR089: 1, AR061: 1
S0007: 1, S0222: 1,
S0049: 1, L0438: 1,
H0520: 1 and L0439: 1. | | | |
| 210 | HODFF88 | 974911 | 220 | 14 - 544 | 833 | His-8 to Gly-18,
Glu-150 to Leu-167. | | | AR054: 34, AR051:
29, AR050: 23, AR089:
4, AR061: 4
H0615: 1 | | | |
| 211 | HOHCE47 | 1216683 | 221 | 629 - 2161 | 834 | Tyr-83 to Ser-92,
Leu-118 to Tyr-123,
Leu-137 to Ser-143, | | | AR061: 1, AR089: 0
S0040: 1, H0580: 1,
S0222: 1, H0355: 1, | | | |

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|-----|---------|--------|-----|-----------|-----|---|---|--|--|
| 214 | HRADM45 | 717358 | 224 | 2 - 472 | 837 | Lys-1 to Leu-6,
Asp-25 to Pro-30. | L0595: 1.
AR089: 14, AR061: 6
H0555: 1 and L0777:
1. | | |
| 215 | HRAED74 | 942527 | 225 | 289 - 651 | 838 | His-9 to Ile-15. | AR061: 1, AR089: 1,
S0222: 3, H0052: 3,
L0361: 3, H0179: 2,
L0769: 2, H0521: 2,
H0555: 2, L0779: 2,
L0758: 2, H0663: 1,
H0549: 1, S0220: 1,
H0586: 1, H0156: 1,
S0010: 1, H0596: 1,
S0051: 1, T0010: 1,
H0271: 1, L0143: 1,
H0617: 1, H0652: 1,
L0764: 1, L0794: 1,
L0806: 1, L0809: 1,
H0518: 1, H0478: 1,
L0751: 1, L0747: 1,
L0750: 1, L0780: 1,
L0731: 1 and L0366: 1. | | |
| 216 | HR0DZ70 | 942673 | 226 | 3 - 440 | 839 | Lys-49 to Lys-54,
Trp-106 to Lys-112,
Leu-130 to Gly-141. | AR089: 12, AR061: 4
H0598: 1 and H0135:
1. | | |
| 217 | HSKAC24 | 823869 | 227 | 98 - 481 | 840 | Ser-1 to Asp-7, | AR061: 2, AR089: 1 | | |

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| 223 | HTMV09 | 909843 | 233 | 1 - 711 | 846 | Asp-22 to Asp-28, Leu-98 to Trp-103, Glu-123 to Trp-154. | AR089: 13, AR061: 13, L0666: 3, L0758: 3, H0616: 2, L0779: 2, S0036: 1, L0598: 1, L0766: 1, L0651: 1, L0806: 1, L0776: 1, H0144: 1, H0547: 1, H0672: 1 and H0555: 1. | | |
| 224 | HTMV66 | 1151075 | 234 | 861 - 175 | 847 | Ile-39 to Ser-46, Val-69 to Gln-75, Phe-90 to Ser-100. | AR061: 5, AR089: 1, H0616: 1 and L0758: 1. | | |
| | | 813038 | 555 | 1 - 318 | 1168 | Ser-38 to Pro-45. | | | |
| 225 | HTGAU79 | 1175071 | 235 | 62 - 976 | 848 | His-12 to Arg-20, Pro-26 to Asp-43, Ala-62 to Glu-70, Arg-78 to Arg-83, Phe-100 to Gln-105, Gly-129 to Glu-136, Met-182 to Gly-190, Tyr-277 to Ala-284. | AR061: 7, AR089: 4, H0551: 3, H0529: 3, L0769: 3, L0758: 3, S0418: 2, L0770: 2, L0773: 2, L0521: 2, H0701: 2, S0126: 2, L0747: 2, L0731: 2, L0759: 2, L0589: 2, L0601: 2, H0624: 1, H0149: 1, H0556: 1, H0295: 1, S0134: 1, H0583: 1, H0661: 1, H0592: 1, H0013: 1, H0635: 1, H0581: 1, | | |

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| | | | | | | | | | S0250: 1, H0212: 1,
H0412: 1, S0144: 1,
L0763: 1, L0645: 1,
L0764: 1, L0794: 1,
L0766: 1, L0775: 1,
L0783: 1, L0665: 1,
H0519: 1, H0435: 1,
H0672: 1, H0436: 1,
S3014: 1, S0028: 1,
L0750: 1, L0777: 1,
L0366: 1, H0667: 1 and
H0423: 1. | | |
| 226 | HTLEJ11 | 973302 | 236 | 2 - 802 | 63 - 977 | 556 | 1169 | His-12 to Arg-20,
Pro-26 to Asp-43,
Ala-62 to Glu-70,
Arg-78 to Arg-83,
Phe-100 to Gln-105,
Gly-129 to Glu-136. | AR061: 3, AR089: 1
H0618: 3 and H0253:
1. | 15q13-qter | |
| 227 | HTLIY52 | 1218691 | 237 | 180 - 1376 | | 850 | Pro-3 to Gly-8,
Val-21 to Gly-30,
Gly-68 to Ala-85,
His-94 to Gly-99, | AR061: 0, AR089: 0
H0618: 64, H0253: 52,
L0758: 6, L0779: 2,
H0392: 1, H0038: 1, | | | |

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| 230 | HUJAD24 | 1161319 | 240 | 770 - 1237 | 853 | Gln-49 to Thr-69,
His-129 to Cys-143. | AR089: 1, AR061: 0
L0750: 3, H0650: 2,
H0637: 2, H0265: 1,
H0556: 1, S0222: 1,
H0040: 1, H0280: 1,
L0655: 1, L0789: 1 and
L0666: 1. | | |
| | | 911498 | 558 | 3 - 293 | 1171 | | | | |
| 231 | HUTSF11 | 966029 | 241 | 3 - 302 | 854 | Glu-1 to Glu-6,
Asn-16 to Arg-22. | AR089: 0, AR061: 0
S0464: 1 and L0356: 1. | | |
| 232 | HUVGZ88 | 1227628 | 242 | 83 - 862 | 855 | Gln-216 to Asp-226,
Thr-250 to Thr-256. | AR089: 2, AR061: 2
L0789: 4, L0758: 4,
H0657: 3, H0052: 3,
L0438: 3, L0744: 3,
L0779: 3, L0005: 2,
H0581: 2, H0194: 2,
H0046: 2, H0038: 2,
L0800: 2, L0659: 2,
H0521: 2, L0743: 2,
L0439: 2, H0556: 1,
S0282: 1, S0358: 1,
H0619: 1, H0586: 1,
H0618: 1, H0231: 1,
S0362: 1, H0622: 1,
T0006: 1, H0616: 1,
H0413: 1, H0623: 1, | | |

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|-----|---------|--------|-----|------------|------|--|--|--|--|--|--|
| | | | | | | | | | L0351: 1, S0150: 1,
L0769: 1, L0372: 1,
L0662: 1, L0794: 1,
L0775: 1, L0651: 1,
L0527: 1, L0657: 1,
L0666: 1, H0547: 1,
H0690: 1, H0658: 1,
H0672: 1, H0539: 1,
S0378: 1, H0555: 1,
L0754: 1, L0747: 1,
L0780: 1, L0596: 1,
S0192: 1, H0542: 1 and
H0423: 1. | | |
| 233 | HWADY66 | 959020 | 559 | 83 - 439 | 1172 | Asn-89 to Asn-95. | | | AR061: 1, AR089: 1
H0581: 1, H0494: 1,
H0521: 1, H0444: 1,
H0543: 1 and L0465: 1. | | |
| 234 | HWAFG04 | 952878 | 244 | 1658 - 789 | 857 | Gln-110 to Asp-120,
Ser-189 to Phe-207,
Cys-218 to Ser-228,,
Gln-240 to Ala-245,
Glu-263 to Ser-271. | | | AR089: 17, AR061: 8
L0789: 4, L0758: 4,
H0657: 3, H0052: 3,
L0438: 3, L0744: 3,
L0779: 3, L0005: 2,
H0581: 2, H0194: 2,
H0046: 2, H0038: 2. | | |

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|-----|---------|---------|-----|---------|-----|--|---|--|--|
| 236 | HWAGS73 | 1150212 | 246 | 1 - 339 | 859 | Val-14 to Lys-21,
Gln-41 to Trp-46,
Ala-98 to Pro-103. | S0114: 1, H0650: 1,
H0255: 1, S0360: 1,
S0278: 1, H0486: 1,
H0318: 1, H0457: 1,
H0039: 1, H0553: 1,
L0763: 1, L0761: 1,
L0764: 1, L0789: 1,
H0144: 1, S0374: 1,
S0310: 1, H0555: 1,
L0758: 1, H0445: 1 and
S0276: 1. | | |
| | | | | | | | AR089: 2, AR061: 2
H0581: 3, H0622: 3,
H0575: 2, H0090: 2,
L0777: 2, L0757: 2,
S0114: 1, H0650: 1,
H0255: 1, S0360: 1,
S0278: 1, H0486: 1,
H0318: 1, H0046: 1,
H0457: 1, H0039: 1,
H0553: 1, L0763: 1,
L0761: 1, L0764: 1,
L0789: 1, H0144: 1,
S0374: 1, S0310: 1,
H0555: 1, L0758: 1,
H0445: 1 and S0276: 1. | | |

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|-----|---------|---------|-----|------------|------|---|---|--|--|
| | | 894404 | 561 | 1 - 339 | 1174 | Val-14 to Lys-21,
Gln-41 to Trp-46,
Ala-98 to Pro-103. | | | |
| 237 | HWLEA48 | 927676 | 247 | 100 - 408 | 860 | Pro-1 to Thr-8. | AR089: 1, AR061: 0
S0354: 1 and L0596: 1. | | |
| 238 | HWLHS82 | 934505 | 248 | 2 - 427 | 861 | Gly-34 to Lys-44,
Glu-113 to Glu-118. | AR089: 2, AR061: 1
L0769: 3, S0354: 1,
H0393: 1, H0355: 1 and
H0124: 1. | | |
| 239 | HWMIB81 | 955336 | 249 | 1491 - 922 | 862 | Ile-94 to Asp-99,
Asp-118 to Pro-123,
Glu-131 to Ile-140,
Tyr-143 to Asp-152,
Glu-169 to Lys-179. | AR061: 1, AR089: 1
L0748: 2, H0171: 1,
S0134: 1, S0354: 1,
S0358: 1, H0014: 1,
H0083: 1, H0510: 1,
L0764: 1, L0803: 1,
L0789: 1, H0593: 1,
H0659: 1, H0539: 1,
H0555: 1, L0751: 1,
L0758: 1, L0759: 1 and
L0595: 1. | | |
| 240 | HCWDV17 | 1105673 | 250 | 32 - 607 | 863 | Ala-144 to Glu-151,
Thr-162 to Thr-168. | AR089: 12, AR061: 6
H0305: 4 | | |
| | | 974478 | 562 | 32 - 697 | 1175 | Ala-144 to Glu-151,
Thr-162 to Thr-168. | | | |
| 241 | HELDI95 | 1103374 | 251 | 49 - 525 | 864 | | AR089: 1, AR061: 1
S0045: 2, S0278: 1, | | |

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|-----|---------|---------|-----|------------|------|--|---|--|--|
| 242 | HAGFO25 | 953059 | 563 | 461 - 895 | 1176 | Arg-71 to Asp-76. | H0191: 1, H0027: 1,
H0644: 1, S0028: 1,
S0031: 1 and S0260: 1. | | |
| | | 1150845 | 252 | 1 - 735 | 865 | Gly-1 to Glu-7,
Gly-30 to Gln-40,
Gly-69 to Gln-75,
Leu-98 to Leu-107,
Tyr-146 to Gly-161,
Arg-179 to Ser-186. | AR061: 9, AR089: 3
L0794: 11, S0010: 3,
S0346: 3, L0791: 2,
L0439: 2, L0758: 2,
S0222: 1, T0060: 1,
H0051: 1, S0388: 1,
H0188: 1, S0214: 1,
H0252: 1, L0666: 1,
L0438: 1, L0743: 1,
L0750: 1, L0779: 1,
S0031: 1, L0480: 1,
L0597: 1 and H0667: 1. | | |
| | | 957992 | 564 | 3 - 728 | 1177 | Gly-26 to Gln-36,
Gly-65 to Gln-71,
Leu-94 to Leu-103. | | | |
| 243 | HAWAB54 | 1149319 | 253 | 1440 - 283 | 866 | Ala-16 to Thr-21,
Arg-76 to Asn-104,
Ala-123 to Glu-129,
Leu-142 to Glu-147,
Gly-170 to Gln-180,
Gly-209 to Gln-215,
Leu-238 to Leu-247, | L0794: 11, S0010: 3,
S0346: 3, L0791: 2,
L0439: 2, L0758: 2,
S0222: 1, T0060: 1,
H0051: 1, S0388: 1,
H0188: 1, S0214: 1,
H0252: 1, L0666: 1, | | |

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|-----|---------|---------|-----|----------|------|--|--|--|--|--|--|--|
| | | | | | | | | | L0771: 1, L0804: 1,
L0805: 1, L0776: 1,
L0657: 1, L0382: 1,
L0809: 1, L0663: 1,
L0665: 1, H0144: 1,
H0691: 1, T0068: 1,
H0520: 1, H0658: 1,
H0648: 1, H0539: 1,
H0521: 1, S0028: 1,
L0744: 1, L0748: 1,
L0779: 1, L0592: 1,
L0604: 1, L0362: 1 and
S0276: 1. | | | |
| 245 | HMALL66 | 1105097 | 255 | 38 - 376 | 868 | Gln-54 to Val-63,
Asn-88 to Pro-93. | AR061: 9, AR089: 3
L0770: 4, H0638: 1,
S0278: 1, H0641: 1,
L0763: 1, L0809: 1,
L0779: 1 and L0758: 1. | | | | | |
| | | 956195 | 566 | 39 - 377 | 1179 | Gln-54 to Val-63,
Asn-88 to Pro-93. | | | | | | |
| 246 | HOACE12 | 858976 | 256 | 2 - 349 | 869 | | AR089: 2, AR061: 1
L0794: 11, S0010: 3,
S0346: 3, L0791: 2,
L0439: 2, L0758: 2,
S0222: 1, T0060: 1,
H0051: 1, S0388: 1, | | | | | |

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|-----|---------|---------|-----|-----------|------|--|--|--|---|--|--|
| | | | | | | | | Lys-58 to Val-63,
Tyr-71 to Val-78. | H0069: 1, H0123: 1,
L0783: 1, H0521: 1 and
L0748: 1. | | |
| 252 | HBINB52 | 974122 | 570 | 298 - 450 | 1183 | | | Gln-20 to Arg-26. | AR061: 4, AR089: 4
H0318: 1, L0766: 1
and L0748: 1. | | |
| | | 1128792 | 262 | 527 - 75 | 875 | | | Leu-16 to Glu-22,
Tyr-89 to Asn-95. | | | |
| | | 726475 | 571 | 160 - 357 | 1184 | | | Pro-15 to Cys-23. | | | |
| 253 | HDABQ83 | 1201703 | 263 | 183 - 1 | 876 | | | Lys-17 to Phe-26,
Gln-30 to Leu-43. | AR089: 4, AR061: 2
L0163: 3, H0497: 2,
L0439: 2, H0662: 1,
S0360: 1, L0717: 1,
S6016: 1, S0051: 1,
H0428: 1, L0662: 1,
L0768: 1, L0774: 1,
L0776: 1, L0656: 1,
L0789: 1, L0666: 1,
L0743: 1, L0749: 1 and
L0777: 1. | | |
| | | 669619 | 572 | 219 - 374 | 1185 | | | Asp-3 to Ser-11. | | | |
| 254 | HDPDC84 | 1226990 | 264 | 82 - 2970 | 877 | | | Lys-32 to Val-61,
Pro-83 to Ala-89,
Lys-114 to Gly-120,
Asn-137 to Arg-147,
Gly-186 to Thr-194,
Val-211 to Glu-227, | AR061: 4, AR089: 1
L0749: 6, L0794: 5,
H0550: 4, H0575: 4,
H0521: 4, L0601: 4,
H0580: 3, L0761: 3,
L0766: 3, H0402: 2, | | |

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|-----|---------|---------|-----|-----------|------|---|---|--|--|
| | | | | | | | L0584: 1 and H0136: 1. | | |
| | | 616980 | 573 | 64 - 528 | 1186 | Lys-32 to Val-61,
Pro-83 to Ala-89. | AR089: 0, AR061: 0
H0436: 11, H0255: 7,
H0559: 7, H0521: 7,
H0254: 4, H0423: 4,
H0265: 3, H0486: 3,
H0250: 3, H0581: 3,
H0271: 3, H0124: 3,
H0264: 3, H0555: 3,
H0341: 2, S0354: 2,
H0580: 2, H0370: 2,
H0586: 2, H0257: 2,
H0069: 2, H0083: 2,
H0031: 2, H0634: 2,
H0488: 2, S0422: 2,
S0426: 2, L0766: 2,
L0649: 2, L0805: 2,
L0653: 2, L0776: 2,
L0655: 2, L0731: 2,
H0445: 2, H0543: 2,
H0677: 2, H0556: 1,
H0584: 1, H0140: 1,
H0583: 1, H0656: 1,
H0402: 1, H0305: 1, | | |
| 255 | HDPUF40 | 1212494 | 265 | 49 - 1713 | 878 | Ala-9 to Glu-20,
Thr-22 to Gly-32,
Gly-57 to Ser-67,
Arg-125 to Ser-138,
Gly-167 to Gly-173,
Ala-289 to Glu-298,
Leu-317 to Ala-323,
Glu-339 to Gly-347,
Leu-358 to Thr-363,
Glu-395 to Arg-411,
Ser-446 to Glu-455,
Glu-475 to Ala-481,
Ser-489 to Leu-497,
Ala-501 to Pro-512,
Asn-520 to Asn-526,
Ser-546 to Glu-553. | | | |

Pro-693 to Ile-700,
Pro-795 to Gly-801.

H0662: 1, H0306: 1,
S0358: 1, S0132: 1,
H0437: 1, H0549: 1,
H0609: 1, H0610: 1,
H0602: 1, H0587: 1,
H0333: 1, H0559: 1,
H0486: 1, H0013: 1,
H0069: 1, H0635: 1,
H0156: 1, H0575: 1,
H0590: 1, H0318: 1,
H0052: 1, H0046: 1,
H0457: 1, H0081: 1,
H0083: 1, H0247: 1,
H0284: 1, H0615: 1,
L0194: 1, H0031: 1,
H0038: 1, H0551: 1,
H0272: 1, H0494: 1,
H0625: 1, H0641: 1,
L0763: 1, L0769: 1,
L0761: 1, L0772: 1,
L0771: 1, L0773: 1,
L0648: 1, L0767: 1,
L0768: 1, L0794: 1,
L0766: 1, L0774: 1,
L0375: 1, L0607: 1,
L0788: 1, L0665: 1,

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|-----|---------|---------|-----|-------------|------|---|--|--|--|
| 262 | HFVIP88 | 697730 | 580 | 2 - 181 | 1193 | Gly-43 to Tyr-50. | S0002: 1, L0631: 1,
L0769: 1, L0372: 1,
L0764: 1, L0768: 1,
L0803: 1, L0783: 1,
L0545: 1, L0791: 1,
L0664: 1, L0665: 1,
H0144: 1, L0438: 1,
H0689: 1, S0380: 1,
S0013: 1, H0696: 1,
H0555: 1, L0743: 1,
L0744: 1, L0747: 1,
L0731: 1, L0759: 1,
L0596: 1 and L0604: 1. | | |
| | | 1124705 | 272 | 96 - 299 | 885 | | AR061: 6, AR089: 2
L0755: 5, H0212: 2,
L0439: 2, L0754: 2,
H0393: 1, H0409: 1,
L0764: 1, L0662: 1,
L0803: 1, L0382: 1,
L0666: 1, L0438: 1,
L0749: 1 and L0752: 1. | | |
| 263 | HGBAS76 | 960741 | 581 | 96 - 299 | 1194 | | | | |
| | | 1193040 | 273 | 1181 - 1603 | 886 | Asn-36 to Gly-43,
Gly-66 to Glu-73,
Ser-86 to Pro-92. | AR089: 1, AR061: 0
L0747: 5, L0439: 3,
L0756: 3, L0775: 2. | | |

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|-----|---------|---------|-----|-----------|------|--|---|--|--|---|
| 265 | HHEHU73 | 1151483 | 275 | 378 - 746 | 888 | Glu-49 to Asn-59,
Lys-70 to Lys-82,
Gly-99 to Cys-116. | AR089: 64, AR061: 15
H0542: 2 | | | |
| 266 | HHEMA11 | 923895 | 584 | 61 - 279 | 1197 | Glu-4 to Leu-11,
Gln-30 to Cys-40,
Pro-53 to Pro-59,
Thr-99 to Ser-104. | AR089: 3, AR061: 1
H0328: 1, L0758: 1
and H0543: 1. | | | |
| | | 1151484 | 276 | 129 - 497 | 889 | Gln-13 to Ile-29. | | | | |
| 267 | HHEQK01 | 966924 | 585 | 129 - 497 | 1198 | Gln-13 to Ile-29. | AR089: 7, AR061: 1
L0589: 1, H0542: 1
and H0543: 1. | | | |
| | | 1107392 | 277 | 195 - 1 | 890 | Gln-1 to Thr-6. | | | | |
| 268 | HHP8M84 | 871911 | 586 | 64 - 249 | 1199 | | AR089: 68, AR061: 29
20q11.2-q12 | | | 139190,
139190,
224100,
600281,
600281,
601002,
601002,
601146,
601146,
601146 |
| | | 915639 | 278 | 2 - 373 | 891 | | | | | |

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|-----|---------|---------|-----|------------|------|--|--|--|--|
| 270 | HIBCC94 | 706739 | 587 | 2 - 496 | 1200 | Asn-1 to Asp-8,
Gly-51 to Ser-64. | H0672: 1, S0328: 1,
S0406: 1, H0187: 1,
L0747: 1, L0749: 1,
L0759: 1 and L0608: 1. | | |
| | | 1161292 | 280 | 806 - 258 | 893 | Cys-12 to Gln-17,
Lys-47 to Thr-57,
Leu-77 to Gly-92,
Gln-153 to Arg-160. | AR089: 1, AR061: 1
L0439: 4, T0010: 1 and
L0352: 1. | | |
| | | 504326 | 588 | 3 - 251 | 1201 | Glu-1 to Arg-6,
Ser-11 to Val-17,
Gln-42 to Arg-54. | | | |
| | | 504330 | 589 | 470 - 132 | 1202 | | | | |
| 271 | HKADN56 | 1220254 | 281 | 370 - 1650 | 894 | Ser-32 to Glu-39,
Ala-60 to Trp-69. | AR089: 7, AR061: 4
L0754: 12, S0360: 8,
S0152: 7, S0358: 6,
H0046: 6, H0100: 5,
L0751: 5, L0777: 5,
L0601: 5, H0052: 4,
L0740: 4, H0051: 3,
H0266: 3, L0526: 3,
S0374: 3, L0779: 3,
H0265: 2, H0556: 2,
H0341: 2, H0661: 2,
H0619: 2, H0050: 2, | | |

H0083: 2, H0622: 2,
H0617: 2, H0673: 2,
T0042: 2, H0529: 2,
L0763: 2, L0770: 2,
L0772: 2, L0373: 2,
L0374: 2, L0771: 2,
L0662: 2, L0768: 2,
L0809: 2, S0126: 2,
H0435: 2, H0658: 2,
S0332: 2, S0027: 2,
L0748: 2, L0750: 2,
L0756: 2, L0755: 2,
L0758: 2, L0589: 2,
L0591: 2, L0603: 2,
H0656: 1, S0282: 1,
H0484: 1, H0638: 1,
S0356: 1, H0580: 1,
S0140: 1, S0222: 1,
S0005: 1, H0574: 1,
H0253: 1, H0390: 1,
H0421: 1, H0194: 1,
H0085: 1, H0263: 1,
T0110: 1, H0597: 1,
H0545: 1, H0009: 1,
H0012: 1, H0057: 1,
H0267: 1, H0179: 1,

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|-----|---------|---------|-----|-----------|------|--|---|--|--|--|
| 282 | HPQSB68 | 1221022 | 292 | 294 - 97 | 905 | Asp-36 to Lys-42. | AR089: 1, AR061: 1
S0136: 2 | | | |
| | | 740087 | 600 | 89 - 247 | 1213 | Leu-7 to Gln-17. | | | | |
| 283 | HRDBH04 | 1150876 | 293 | 329 - 724 | 906 | Thr-56 to Gly-62,
Glu-72 to Gly-81. | AR089: 7, AR061: 6
L0769: 16, L0776: 16,
L0742: 13, L0745: 13,
L0754: 12, L0748: 11,
L0439: 11, L0747: 10,
L0805: 8, L0438: 6,
L0731: 6, L0764: 5,
L0806: 5, L0749: 5,
L0779: 5, L0752: 5,
L0771: 4, H0052: 3,
L0796: 3, L0761: 3,
L0741: 3, L0756: 3,
L0753: 3, L0758: 3,
S0360: 2, H0013: 2,
H0068: 2, T0041: 2,
L0768: 2, L0659: 2,
L0783: 2, L0809: 2,
H0670: 2, L0746: 2,
L0591: 2, H0265: 1,
H0686: 1, H0583: 1,
H0657: 1, L0785: 1,
H0662: 1, S0418: 1, | | | |

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|-----|---------|---------|-----|------------|------|--|---|--|--|--|--|
| | | | | | | | | | L0743: 1, L0777: 1,
L0780: 1, L0755: 1,
L0757: 1, L0759: 1,
L0603: 1, S0026: 1,
H0543: 1 and H0352: 1. | | |
| 284 | HSICR69 | 922022 | 601 | 285 - 680 | 1214 | Thr-56 to Gly-62,
Glu-72 to Gly-81. | Thr-48 to Arg-54,
Pro-149 to Ser-155. | AR089: 2, AR061: 1
H0036: 2 | | | |
| | | 531061 | 602 | 127 - 273 | 1215 | Ser-14 to Lys-19. | | | | | |
| | | 1105417 | 295 | 713 - 438 | 908 | | | AR061: 8, AR089: 7
H0590: 1, L0766: 1,
L0659: 1, L0608: 1 and
L0362: 1. | | | |
| 286 | HSYBL15 | 793624 | 603 | 117 - 284 | 1216 | | | | | | |
| | | 1104299 | 296 | 2 - 931 | 909 | Pro-26 to Gly-32,
Ala-133 to Cys-138,
Asp-145 to Lys-152,
Leu-164 to Ser-173,
Lys-178 to Ser-183,
Asp-260 to Phe-266. | AR061: 1, AR089: 0
S0212: 1, H0551: 1 and
L0366: 1. | | | | |
| | | 660053 | 604 | 2 - 286 | 1217 | Pro-26 to Gly-32. | | | | | |
| 287 | HTEKH29 | 855660 | 297 | 478 - 2028 | 910 | Ser-27 to Glu-35,
Thr-43 to Phe-52,
Val-59 to Gln-70,
His-74 to Val-79. | AR089: 8, AR061: 7 | | | | |

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Ala-130 to Phe-141,
Val-145 to Ala-151,
Asp-159 to Glu-165,
Ser-185 to Lys-191. | | | | |
| 288 | HTGEL46 | 1151520 | 298 | 331 - 705 | 911 | | Glu-55 to His-72. | | AR089: 0, AR061: 0
S0218: 1, H0264: 1 and
S0053: 1. | | |
| | | 685425 | 605 | 323 - 457 | 1218 | | | | | | |
| 289 | HTGFA05 | 1198110 | 299 | 3 - 1262 | 912 | | Ile-45 to Arg-52,
Phe-77 to Pro-85,
Leu-111 to Val-118,
Ile-124 to Thr-129,
Pro-139 to Gly-151,
Arg-186 to Gly-215,
Lys-223 to Glu-230. | | AR061: 1, AR089: 0
H0556: 10, L0748: 8,
H0620: 7, L0747: 7,
L0637: 5, H0265: 4,
H0013: 4, H0551: 4,
L0776: 4, L0663: 4,
L0596: 4, H0622: 3,
H0617: 3, L0772: 3,
L0766: 3, S0126: 3,
L0751: 3, L0752: 3,
S0031: 3, L0593: 3,
H0657: 2, S0360: 2,
S0222: 2, T0115: 2,
H0009: 2, L0471: 2,
H0594: 2, H0288: 2,
H0039: 2, H0424: 2,
H0135: 2, H0040: 2, | | |

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| | H0623: 2, L0763: 2,
L0769: 2, L0796: 2,
L0804: 2, L0775: 2,
L0634: 2, L0666: 2,
L0438: 2, L0756: 2,
L0757: 2, H0445: 2,
L0595: 2, H0542: 2,
H0423: 2, H0422: 2,
T0002: 1, S0114: 1,
S0218: 1, H0661: 1,
S0358: 1, S0007: 1,
S0046: 1, S0132: 1,
S0278: 1, H0431: 1,
H0370: 1, H0586: 1,
H0632: 1, H0486: 1,
T0040: 1, S0280: 1,
H0318: 1, H0581: 1,
H0085: 1, T0110: 1,
H0545: 1, H0081: 1,
S0362: 1, H0247: 1,
H0266: 1, H0290: 1,
H0292: 1, H0286: 1,
S0340: 1, S0036: 1,
H0090: 1, H0591: 1,
H0038: 1, H0616: 1,
H0433: 1, H0412: 1, |
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|-----|---------|---------|-----|-----------|------|---|--|--|--|
| 290 | HTLDU61 | 1165319 | 300 | 690 - 220 | 913 | Cys-59 to Thr-68,
Ile-78 to Thr-83,
Pro-93 to Gly-105,
Arg-140 to Gly-169,
Lys-177 to Glu-184. | AR061: 2, AR089: 2
H0253: 1, S0010: 1,
L0456: 1, H0695: 1 and
L0657: 1. | | |
| | | 530316 | 607 | 63 - 224 | 1220 | Gln-5 to His-17,
Pro-30 to Ser-40,
Pro-42 to Thr-65,
Gly-102 to Gln-107,
Ala-112 to Lys-118,
Ser-127 to Thr-138. | | | |
| 291 | HTOFT34 | 1152490 | 301 | 361 - 609 | 914 | | AR089: 8, AR061: 5
H0264: 2 and L0367:
1. | | |
| | | 527144 | 608 | 106 - 270 | 1221 | | | | |
| 292 | HTTDH46 | 1152491 | 302 | 2 - 1144 | 915 | Gly-50 to Asp-59,
Thr-220 to Phe-233,
Glu-285 to Tyr-291,
Thr-298 to Arg-303,
Ala-353 to Asn-358. | AR061: 7, AR089: 2
H0253: 10, H0617: 8,
H0559: 7, H0265: 6,
H0618: 5, H0551: 5,
H0052: 4, H0620: 4,
L0794: 4, H0556: 3,
H0135: 3, H0087: 3,
L0659: 3, L0666: 3,
L0663: 3, L0438: 3,
H0522: 3, L0749: 3, | | |

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| | | H0581: 1, H0194: 1,
H0327: 1, H0046: 1,
H0009: 1, H0178: 1,
H0012: 1, H0023: 1,
H0201: 1, S0051: 1,
H0083: 1, S6028: 1,
H0266: 1, H0271: 1,
H0428: 1, H0604: 1,
H0417: 1, H0181: 1,
H0163: 1, H0038: 1,
H0634: 1, H0063: 1,
H0264: 1, H0412: 1,
S0038: 1, L0351: 1,
H0359: 1, S0150: 1,
H0646: 1, H0538: 1,
S0002: 1, S0426: 1,
L0640: 1, L0772: 1,
L0372: 1, L0641: 1,
L0643: 1, L0764: 1,
L0767: 1, L0768: 1,
L0766: 1, L0375: 1,
L0378: 1, L0806: 1,
L0652: 1, L0656: 1,
L0636: 1, L0790: 1,
L0664: 1, H0144: 1,
S0374: 1, H0520: 1, | | | | | |
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|-----|---------|-------------------|------------|------------------------|-------------|------------------|--|--|--|
| 293 | HTTIO05 | 951114
1229905 | 609
303 | 3 - 500
1367 - 1624 | 1222
916 | Arg-I to Thr-15. | H0547: 1, H0593: 1,
H0682: 1, H0651: 1,
S0328: 1, H0539: 1,
S0380: 1, S0332: 1,
S3014: 1, S0027: 1,
L0754: 1, L0750: 1,
L0755: 1, L0757: 1,
L0758: 1, S0031: 1,
L0593: 1, H0667: 1,
H0217: 1, H0423: 1,
H0422: 1 and S0042: 1. | | |
| | | 931037 | 610 | 1286 - 1564 | 1223 | | AR061: 57, AR089: 49
L0770: 2, S0114: 1,
L0717: 1, H0634: 1,
L0773: 1, L0521: 1,
L0803: 1, L0791: 1,
L0664: 1, S0330: 1,
S0380: 1, L0759: 1 and
H0653: 1. | | |
| 294 | HWHGY45 | 911621 | 304 | 3 - 203 | 917 | | AR089: 23, AR061: 3
S0144: 2, H0662: 1,
H0586: 1, H0587: 1,
T0060: 1, H0696: 1 and
L0745: 1. | | |

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|-----|---------|-------------------|------------|-----------------------|-------------|--|--|--|--|
| 295 | HWLQR48 | 1128304 | 305 | 338 - 508 | 918 | | AR089: 23, AR061: 6
L0518: 4, L0731: 3,
L0637: 2, H0659: 2,
H0170: 1, S6024: 1,
S0360: 1, H0586: 1,
H0050: 1, L0598: 1,
L0763: 1, L0666: 1,
L0663: 1, L0743: 1,
L0745: 1 and L0601: 1. | | |
| 296 | HWLQX76 | 914556
1152280 | 611
306 | 338 - 475
2 - 466 | 1224
919 | Gly-1 to Pro-6,
His-18 to Ser-23,
Asn-45 to Thr-56,
Ala-65 to Arg-70,
Asp-84 to Ile-89,
Glu-109 to Leu-114,
Lys-146 to Lys-155. | AR089: 1, AR061: 1
H0553: 3, S0360: 1,
H0561: 1, L0526: 1,
H0519: 1, S0126: 1,
H0543: 1 and L0697: 1. | | |
| 297 | HATDD09 | 894607
1165331 | 612
307 | 1 - 996
428 - 1027 | 1225
920 | His-12 to Ser-17,
Asn-39 to Thr-50,
Ala-59 to Arg-64,
Asp-78 to Ile-83.
Ser-25 to Asp-40,
Pro-47 to Glu-54,
Pro-146 to Gly-153,
Pro-194 to Thr-200. | AR061: 4, AR089: 4
L0361: 2, H0662: 1,
T0039: 1, H0156: 1,
H0052: 1, H0194: 1,
H0179: 1, H0135: 1, | | |

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|-----|---------|-------------------|------------|---------------------|-------------|---|---|--|--|--|--|
| | | | | | | | | | L0662: 1, L0364: 1,
L0790: 1, L0666: 1,
S0028: 1 and S0194: 1. | | |
| 298 | HBIGT03 | 573794
1105484 | 613
308 | 2 - 184
352 - 89 | 1226
921 | Ser-33 to Ala-47. | AR061: 5, AR089: 3
L0769: 2, H0318: 1
and L0787: 1. | | | | |
| | | 923800 | 614 | 35 - 226 | 1227 | Ala-16 to Ser-22,
Pro-31 to Leu-38,
Ser-41 to Gly-48. | | | | | |
| 299 | HMTMF45 | 1141737 | 309 | 33 - 401 | 922 | | AR061: 1, AR089: 1
L0766: 3, L0777: 2,
S0116: 1, S0376: 1,
H0457: 1, L0771: 1,
L0803: 1, L0804: 1,
L0657: 1, L0659: 1,
H0525: 1 and L0750: 1. | | | | |
| | | 553382 | 615 | 2 - 376 | 1228 | Arg-3 to Asp-14,
Glu-53 to Gly-59,
Asp-105 to Asn-113. | | | | | |
| 300 | HHPDV86 | 522953 | 310 | 1 - 636 | 923 | Thr-6 to Asp-14,
Ser-36 to Glu-41,
Ala-159 to Trp-168,
Ser-176 to Lys-181. | AR061: 7, AR089: 3
L0809: 3, L0747: 3,
S0360: 2, H0422: 2,
H0556: 1, S0040: 1,
H0664: 1, S0358: 1,
T0048: 1, H0051: 1, | | | | |

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|-----|---------|--------|-----|-----------|-----|---|--|--|---|--|--|--|
| | | | | | | | | | L0794: 1, L0791: 1,
L0664: 1, S0052: 1,
S0053: 1, H0701: 1,
H0689: 1, H0690: 1,
H0521: 1, H0626: 1 and
L0595: 1. | | | |
| 301 | HE8BT56 | 732602 | 311 | 45 - 377 | 924 | | | | AR061: 3, AR089: 2
L0766: 7, L0439: 3,
L0749: 3, H0013: 2,
L0776: 2, L0740: 2,
L0746: 2, H0083: 1,
H0366: 1, S0422: 1,
L0787: 1, L0791: 1,
L0779: 1, L0780: 1 and
L0752: 1. | | | |
| 302 | HUJDH06 | 907613 | 312 | 304 - 672 | 925 | Pro-10 to Lys-22. | | | AR089: 1, AR061: 1
H0650: 1, H0591: 1
and S0390: 1. | | | |
| 303 | HOEIG61 | 907614 | 313 | 174 - 671 | 926 | Lys-31 to Ser-37,
Leu-112 to Ser-119. | | | AR061: 7, AR089: 2
L0769: 3, L0766: 2,
L0638: 1, S0126: 1,
H0683: 1, L0745: 1 and
H0506: 1. | | | |
| 304 | HE8PN24 | 907620 | 314 | 2 - 724 | 927 | Gly-59 to Glt-66,
Cys-87 to Asn-93,
Asn-122 to Trp-127, | | | AR061: 2, AR089: 0
H0013: 2, S0142: 2,
L0740: 1 and L0747: 1. | | | |

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|-----|---------|--------|-----|----------|-----|--|---|--|---|---------|--|---------|
| | | | | | | | Arg-129 to Ser-134,
Ala-144 to Asp-149,
Asn-176 to Ala-182. | | | | | |
| 305 | HGBHI37 | 909745 | 315 | 2 - 451 | 928 | | Ala-1 to Gly-10. | | AR089: 1, AR061: 1
H0656: 1 and H0014:
1. | | | |
| 306 | HCHOK82 | 909755 | 316 | 1 - 1089 | 929 | | Leu-52 to Leu-66,
Trp-97 to Leu-103. | | AR089: 4, AR061: 3
H0457: 3, H0271: 3,
H0543: 3, H0422: 2,
H0583: 1, H0650: 1,
H0484: 1, H0483: 1,
S0442: 1, H0580: 1,
S0140: 1, H0486: 1,
H0250: 1, H0050: 1,
H0630: 1, H0264: 1,
H0488: 1, H0487: 1,
S0002: 1, L0439: 1,
H0707: 1, H0136: 1 and
H0677: 1. | | | |
| 307 | HFPCH24 | 912608 | 317 | 2 - 352 | 930 | | Thr-5 to Asn-13,
Pro-69 to Ala-76. | | AR061: 3, AR089: 3
L0803: 3, S0222: 1,
L0021: 1, H0510: 1,
L0774: 1, L0777: 1,
L0731: 1, S0260: 1 and
S0434: 1. | | | |
| 308 | HTTKF86 | 912689 | 318 | 2 - 223 | 931 | | Arg-9 to Pro-16. | | AR061: 4, AR089: 3 | 22q13.1 | | 103050, |

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|-----|---------|--------|-----|-----------|-----|--|--|--|--|
| 310 | HDTBJ28 | 912714 | 320 | 533 - 243 | 933 | | AR089: 38, AR061: 25
H0393: 1 and H0486: 1. | | |
| 311 | HDPBF48 | 912783 | 321 | 3 - 809 | 934 | Asp-52 to Thr-62,
Thr-101 to Trp-112,
Gly-131 to Asn-141,
Asp-173 to Ile-179. | AR089: 8, AR061: 3
L0758: 4, H0521: 3,
L0163: 2, L0783: 2,
L0749: 2, S0342: 1,
L0021: 1, H0318: 1,
H0373: 1, H0083: 1,
H0674: 1, H0494: 1,
H0529: 1, L0768: 1,
L0790: 1, H0519: 1,
S0126: 1, H0670: 1,
L0602: 1, L0748: 1,
L0777: 1, L0752: 1,
L0759: 1, L0588: 1,
H0542: 1 and H0422: 1. | | |
| 312 | HTPFY55 | 912928 | 322 | 117 - 563 | 935 | Val-14 to Val-19,
Ser-27 to Ser-32. | AR089: 3, AR061: 2
H0039: 1, H0622: 1
and H0644: 1. | | |
| 313 | HMSCM47 | 923632 | 323 | 2 - 685 | 936 | Gln-13 to Lys-19,
Gln-59 to Tyr-69,
Asp-116 to His-126,
Gly-164 to Lys-170,
Gln-182 to Gly-187,
Tyr-207 to Gly-212. | AR089: 6, AR061: 3
H0521: 3, L0794: 2,
L0805: 2, H0520: 2,
L0602: 2, L0756: 2,
H0170: 1, H0556: 1,
S0134: 1, S0116: 1, | | |

H0341: 1, H0662: 1,
S0354: 1, S0360: 1,
H0580: 1, H0619: 1,
S0278: 1, H0574: 1,
H0599: 1, H0590: 1,
H0596: 1, L0471: 1,
H0024: 1, H0014: 1,
L0163: 1, H0051: 1,
H0510: 1, H0615: 1,
H0644: 1, H0617: 1,
H0068: 1, L0060: 1,
H0551: 1, S0450: 1,
S0002: 1, L0369: 1,
L0763: 1, L0371: 1,
L0631: 1, L0637: 1,
L0800: 1, L0764: 1,
L0363: 1, L0767: 1,
L0549: 1, L0803: 1,
L0774: 1, L0776: 1,
L0809: 1, L0791: 1,
H0144: 1, H0658: 1,
H0522: 1, H0478: 1,
S3014: 1, S0028: 1,
L0747: 1, L0749: 1,
L0752: 1, L0753: 1,
L0731: 1, L0758: 1,

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|-----|----------|--------|-----|---------|-----|------------------------------------|--|--|--|
| 315 | HTPCQ24 | 925349 | 325 | 1 - 450 | 938 | Gly-1 to Leu-26, Thr-28 to Leu-35. | L0595: 1 and S0011: 1.
AR061: 2, AR089: 1
H0046: 21, L0747: 10,
H0039: 3, H0024: 2,
L0766: 2, L0654: 2,
L0748: 2, L0439: 2,
L0779: 2, L0777: 2,
T0049: 1, S0212: 1,
H0662: 1, S0354: 1,
S0045: 1, H0393: 1,
H0107: 1, H0266: 1,
S0250: 1, H0615: 1,
H0688: 1, H0040: 1,
H0616: 1, H0551: 1,
H0641: 1, L0770: 1,
L0637: 1, L0764: 1,
L0767: 1, L0768: 1,
L0659: 1, L0647: 1,
L0666: 1, S0027: 1,
S0028: 1, L0743: 1,
L0749: 1, L0750: 1,
L0780: 1, L0755: 1,
L0758: 1 and L0759: 1. | | |
| 316 | HWAIEI37 | 929481 | 326 | 2 - 415 | 939 | | AR089: 5, AR061: 1
H0581: 1 and H0519: 1. | | |

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|-----|---------|--------|-----|----------|-----|--|---|--|--|
| 317 | HDPSF03 | 969536 | 327 | 1 - 1269 | 940 | | AR089: 9, AR061: 3 | | |
| 318 | HLHST63 | 581528 | 328 | 28 - 423 | 941 | Ala-1 to Gly-15,
Arg-32 to Ser-38,
Thr-62 to His-68,
Ser-104 to Thr-110,
Gly-117 to Thr-122. | L0731: 28, L0740: 22,
L0747: 21, L0748: 20,
S0003: 18, L0754: 17,
L0438: 12, L0439: 12,
L0775: 11, L0752: 11,
S0026: 11, L0770: 10,
H0521: 10, L0749: 9,
S0358: 8, L0766: 8,
L0659: 8, L0591: 8,
S0192: 8, S0360: 7,
L0764: 7, H0522: 7,
S0010: 6, H0039: 6,
S0002: 6, L0666: 6,
L0665: 6, H0144: 6,
S0126: 6, L0750: 6,
L0755: 6, L0758: 6,
S0426: 5, L0662: 5,
L0663: 5, L0759: 5,
L0599: 5, T0049: 4,
S0282: 4, H0402: 4,
S0354: 4, H0619: 4,
H0620: 4, H0266: 4,
H0032: 4, H0641: 4,
S0422: 4, L0771: 4, | | |

H0318: 2, H0052: 2,
H0309: 2, H0263: 2,
H0046: 2, S0050: 2,
S0022: 2, S0214: 2,
H0428: 2, H0622: 2,
H0031: 2, H0553: 2,
H0673: 2, H0169: 2,
S0036: 2, H0090: 2,
H0087: 2, H0264: 2,
H0413: 2, H0560: 2,
S0144: 2, L0598: 2,
L0369: 2, L0520: 2,
L0774: 2, L0806: 2,
L0517: 2, L0809: 2,
H0519: 2, H0658: 2,
H0648: 2, H0672: 2,
S0350: 2, S0044: 2,
S0027: 2, L0779: 2,
S0260: 2, H0445: 2,
L0596: 2, L0588: 2,
L0592: 2, L0581: 2,
L0601: 2, L0600: 2,
H0265: 1, H0686: 1,
H0685: 1, S0040: 1,
S0342: 1, S6024: 1,
S0134: 1, H0650: 1,

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|---------------------|---------------------|---------------------|---------------------|---------------------|---------------------|---------------------|---------------------|---------------------|---------------------|---------------------|---------------------|---------------------|---------------------|---------------------|---------------------|---------------------|---------------------|---------------------|---------------------|---------------------|---------------------|---------------------|---------------------|---------------------|---------------------|
| S0116: 1, H0341: 1, | H0661: 1, H0177: 1, | H0306: 1, S0418: 1, | S0356: 1, H0208: 1, | S0046: 1, H0645: 1, | H0393: 1, S0300: 1, | L0717: 1, S6014: 1, | H0438: 1, H0586: 1, | H0333: 1, H0331: 1, | H0632: 1, L0622: 1, | H0486: 1, T0040: 1, | L0586: 1, T0060: 1, | H0244: 1, H0599: 1, | H0098: 1, H0590: 1, | H0004: 1, H0581: 1, | H0421: 1, S0049: 1, | H0196: 1, L2250: 1, | H0235: 1, H0596: 1, | T0115: 1, T0110: 1, | H0597: 1, H0546: 1, | H0545: 1, H0150: 1, | H0009: 1, H0178: 1, | H0123: 1, L0471: 1, | H0012: 1, H0014: 1, | H0015: 1, H0373: 1, | S0388: 1, T0010: 1, |
|---------------------|---------------------|---------------------|---------------------|---------------------|---------------------|---------------------|---------------------|---------------------|---------------------|---------------------|---------------------|---------------------|---------------------|---------------------|---------------------|---------------------|---------------------|---------------------|---------------------|---------------------|---------------------|---------------------|---------------------|---------------------|---------------------|

1. The first column contains the number of the record.
 2. The second column contains the name of the record.
 3. The third column contains the date of the record.
 4. The fourth column contains the time of the record.
 5. The fifth column contains the location of the record.
 6. The sixth column contains the status of the record.
 7. The seventh column contains the type of the record.
 8. The eighth column contains the category of the record.
 9. The ninth column contains the sub-category of the record.
 10. The tenth column contains the sub-sub-category of the record.

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|-----|---------|--------|-----|----------|------|-------------------|--|--|--|
| 319 | HFAAJ44 | 646715 | 616 | 151 - 20 | 1229 | Cys-11 to His-18. | L0606: 1, L0657: 1,
L0493: 1, L0518: 1,
L0782: 1, L0545: 1,
L0529: 1, L0647: 1,
L0792: 1, L0532: 1,
S0148: 1, H0547: 1,
H0593: 1, H0365: 1,
H0689: 1, H0682: 1,
H0684: 1, H0435: 1,
H0670: 1, H0666: 1,
S0380: 1, L0602: 1,
S0152: 1, S0013: 1,
S0146: 1, H0555: 1,
H0478: 1, H0540: 1,
S3012: 1, S0037: 1,
S0206: 1, L0756: 1,
L0777: 1, H0444: 1,
H0595: 1, L0589: 1,
S0011: 1, H0668: 1,
H0665: 1, H0667: 1,
S0194: 1, S0276: 1,
H0542: 1, S0384: 1,
H0506: 1 and H0352: 1. | | |
| | | 744764 | 617 | 39 - 221 | 1230 | | | | |
| | | 489201 | 329 | 3 - 299 | 942 | | | | |
| | | | | | | | AR089: 4, AR061: 4 | | |

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|-----|---------|--------|-----|-----------|-----|---|--|-------|------------------------------|
| 322 | HFTAR20 | 670041 | 332 | 3 - 443 | 945 | | AR089: 6, AR061: 4
L0749: 6, L0794: 4,
H0123: 1, L0768: 1 and
S0194: 1. | | |
| 323 | HCUFD32 | 699379 | 333 | 1 - 498 | 946 | Thr-1 to Leu-11,
Lys-24 to Ile-29,
Gln-134 to Asn-144,
Gln-150 to Thr-165. | AR089: 7, AR061: 3
L0754: 6, L0439: 2,
L0751: 2, L0747: 2,
H0661: 1, H0402: 1,
H0272: 1, L0438: 1,
H0696: 1 and L0779: 1. | | |
| 324 | HKAEO39 | 705332 | 334 | 2 - 463 | 947 | Lys-20 to Ser-28,
Arg-44 to Ala-52,
Leu-83 to Glu-89. | AR089: 0, AR061: 0
L0792: 2, S0420: 1,
H0645: 1, H0494: 1,
L0806: 1, L0807: 1,
L0740: 1 and L0752: 1. | | |
| 325 | HLWBR95 | 734474 | 335 | 3 - 476 | 948 | | AR089: 3, AR061: 1
S0420: 1, H0550: 1,
H0587: 1, H0485: 1,
H0150: 1, H0553: 1,
T0042: 1, L0530: 1 and
S0152: 1. | 10q23 | 174900,
236730,
601493 |
| 326 | HPWCJ63 | 772553 | 336 | 148 - 807 | 949 | Lys-213 to Gly-220. | AR054: 2, AR051: 1,
AR061: 0, AR089: 0,
AR050: 0
S0001: 1, H0191: 1 and
S0044: 1. | | |

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|-----|---------|--------|-----|------------|------|---|---|--|--|
| 327 | HBXCM35 | 957495 | 618 | 1239 - 580 | 1231 | Lys-213 to Gly-220. | AR089: 8, AR061: 4
L0743: 2, S0040: 1,
H0663: 1, H0427: 1,
H0545: 1, S0250: 1,
H0087: 1, S0038: 1,
L0804: 1 and L0783: 1. | | |
| 328 | HULBN83 | 857836 | 338 | 1 - 636 | 951 | | AR089: 1, AR061: 1
H0619: 2, L0779: 2,
S0222: 1, H0530: 1,
H0433: 1, L0766: 1 and
L0753: 1. | | |
| 329 | HAGET77 | 885265 | 339 | 86 - 850 | 952 | Lys-26 to Gln-36,
Leu-50 to Glu-56,
Gly-93 to Thr-106,
Gln-108 to Gly-122,
Gly-132 to Gln-138,
Ser-144 to Trp-153,
Glu-155 to Glu-171,
Lys-178 to Pro-198,
Val-207 to Asn-230,
Arg-235 to Asp-247. | AR061: 4, AR089: 2
S0010: 3, S0036: 3,
L0766: 3, S0222: 2,
S0346: 2, H0310: 2,
H0327: 2, H0457: 2,
H0656: 1, S0282: 1,
S6016: 1, S0665: 1,
L2250: 1, H0051: 1,
S0386: 1, H0342: 1,
S0031: 1, L0366: 1 and
H0543: 1. | | |
| 330 | HMSOZ55 | 910911 | 340 | 3 - 503 | 953 | Lys-22 to Gly-27. | AR089: 6, AR061: 3
S0282: 1, T0040: 1,
H0013: 1, S0182: 1, | | |

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|-----|---------|--------|-----|-----------|-----|--|--|---|--|--|
| 331 | HAPOR42 | 911292 | 341 | 6 - 701 | 954 | | | S0426: 1, H0670: 1,
H0667: 1 and H0542: 1. | | |
| 332 | HMVAU10 | 911449 | 342 | 2 - 538 | 955 | | | AR089: 21, AR061: 10
H0156: 1, H0575: 1,
H0590: 1, H0263: 1 and
L0362: 1. | | |
| 333 | HTTFY29 | 911454 | 343 | 3 - 644 | 956 | | Arg-37 to Arg-44,
Asn-47 to Glu-56,
Lys-65 to Glu-70,
Arg-78 to Pro-83,
Gln-98 to Asp-106,
Pro-142 to Ile-151,
Ala-154 to Thr-180. | AR054: 16, AR051:
13, AR061: 8, AR089:
3, AR050: 1
H0040: 1, H0022: 1,
S0152: 1 and H0521: 1. | | |
| 334 | HHFY06 | 911456 | 344 | 81 - 584 | 957 | | Glu-11 to Ser-21,
Asn-52 to Ser-57,
Arg-81 to Met-88,
Glu-139 to Tyr-146,
Glu-153 to Leu-159. | AR089: 10, AR061: 6
H0619: 1, S0036: 1,
H0135: 1 and H0520: 1. | | |
| 335 | HPCIK72 | 911459 | 345 | 283 - 2 | 958 | | | AR089: 1, AR061: 0
S0358: 1, H0642: 1 and
H0264: 1. | | |
| 336 | HFIDT84 | 919878 | 346 | 64 - 2151 | 959 | | Asp-51 to His-60,
Thr-105 to Pro-117,
Asp-143 to Ala-151, | AR089: 9, AR061: 5
S0192: 2, S0222: 1,
H0562: 1, H0373: 1 and | | |

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| | | | | | L0766: 2, L0776: 2,
L0663: 2, L0565: 2,
S0027: 2, L0742: 2,
L0754: 2, L0750: 2,
L0753: 2, L0759: 2,
L0588: 2, L0362: 2,
H0624: 1, L0002: 1,
H0656: 1, S0212: 1,
S0420: 1, S0356: 1,
H0441: 1, L0034: 1,
L0738: 1, H0546: 1,
H0012: 1, H0620: 1,
H0024: 1, H0014: 1,
H0083: 1, H0622: 1,
T0006: 1, H0617: 1,
H0068: 1, H0090: 1,
H0063: 1, H0334: 1,
H0561: 1, S0150: 1,
H0633: 1, L0372: 1,
L0662: 1, L0804: 1,
L0774: 1, L0656: 1,
L0636: 1, L0635: 1,
L0783: 1, L0384: 1,
L0809: 1, L0528: 1,
L0666: 1, L0664: 1,
H0144: 1, H0547: 1, | | | | |
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| 341 | HEAAE08 | 959970 | 351 | 133 - 621 | 964 | Pro-1 to Pro-12,
Pro-53 to Gly-58,
Gly-65 to Ser-71,
Gly-106 to Lys-111,
Lys-143 to Gly-163. | S0152: 1, S0260: 1 and
L0366: 1.
AR061: 10, AR089: 4
L0789: 6, L0809: 2,
H0669: 1, H0369: 1,
H0252: 1, L0055: 1,
L0763: 1, L0770: 1,
L0638: 1, L0803: 1,
L0805: 1, L0776: 1,
L0753: 1, L0758: 1,
L0592: 1 and H0543: 1. | | |
| 342 | HDPLU91 | 963199 | 352 | 2 - 748 | 965 | Pro-53 to Val-58,
Pro-85 to Ser-95,
Gln-132 to Gly-138. | AR089: 16, AR061: 5
L0439: 10, L0526: 6,
L0005: 5, L0740: 5,
S0422: 4, L0438: 4,
L0758: 4, L0581: 4,
H0370: 3, H0486: 3,
S0003: 3, H0144: 3,
H0659: 3, H0672: 3,
L0744: 3, L0754: 3,
L0731: 3, L0595: 3,
H0657: 2, H0664: 2,
S0418: 2, S0376: 2,
H0431: 2, H0050: 2,
L0471: 2, H0083: 2,
H0266: 2, H0090: 2, | | |

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| 343 | HAPRM21 | 963200 | 353 | 1 - 630 | 966 | Gln-8 to Gly-14,
Thr-164 to Gly-183,
Pro-197 to Asp-210. | AR089: 25, AR061: 5
H0123: 2, L0754: 2,
H0650: 1, H0550: 1. | AR089: 25, AR061: 5
H0123: 2, L0754: 2,
H0650: 1, H0550: 1. | |
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| 344 | HTDAB30 | 965320 | 354 | 3 - 944 | 967 | H0244: 1, H0427: 1,
H0575: 1, S0010: 1 and
L0698: 1.
AR089: 5, AR061: 4
S0152: 7, L0748: 7,
L0779: 6, L0766: 5,
H0591: 4, L0771: 4,
L0749: 4, L0777: 4,
L0759: 4, H0556: 3,
L0803: 3, L0783: 3,
H0521: 3, L0754: 3,
L0731: 3, L0595: 3,
H0423: 3, H0170: 2,
H0657: 2, H0341: 2,
H0013: 2, H0598: 2,
H0412: 2, H0494: 2,
L0768: 2, L0526: 2,
L0663: 2, S0328: 2,
L0755: 2, L0757: 2,
H0542: 2, S0420: 1,
S0358: 1, S0408: 1,
H0619: 1, H0587: 1,
H0486: 1, T0060: 1,
H0575: 1, H0036: 1,
H0318: 1, H0581: 1,
H0434: 1, H0544: 1, | | |
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| 347 | HADEX52 | 971351 | 357 | 38 - 1354 | 970 | Arg-11 to Arg-18,
Glu-23 to Glu-28,
Asn-40 to Leu-45,
Thr-53 to Asp-58,
Lys-74 to Asp-82,
Val-92 to Glu-97, | S0418: 1, S0358: 1,
S0376: 1, S0360: 1,
S0132: 1, H0642: 1,
H0590: 1, H0150: 1,
H0620: 1, H0023: 1,
H0356: 1, H0424: 1,
H0213: 1, H0617: 1,
H0169: 1, H0634: 1,
H0063: 1, T0067: 1,
H0488: 1, H0334: 1,
S0370: 1, H0652: 1,
L0645: 1, L0773: 1,
L0648: 1, L0806: 1,
L0776: 1, L0541: 1,
L0789: 1, L0790: 1,
L0664: 1, S0374: 1,
H0689: 1, H0666: 1,
H0672: 1, H0478: 1,
L0748: 1, L0779: 1,
S0436: 1 and H0506: 1. | | |
| | | | | | | | AR054: 40, AR050:
30, AR051: 28, AR089:
1, AR061: 1
S0270: 8, S0268: 7,
L0731: 4, L0471: 3,
H0201: 2, H0547: 2, | | |

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| | | | | | | Ser-104 to Asn-109,
Asp-127 to Phe-133,
Gln-158 to Asp-170,
Asn-177 to Ala-207. | S0274: 2, L0754: 2,
L0604: 2, S0202: 1,
S0252: 1, S0360: 1,
H0550: 1, H0600: 1,
H0333: 1, H0486: 1,
H0013: 1, H0427: 1,
H0599: 1, H0575: 1,
S0010: 1, H0194: 1,
H0327: 1, H0569: 1,
H0594: 1, S6028: 1,
S0250: 1, H0622: 1,
L0544: 1, H0144: 1,
L0438: 1, H0519: 1,
S0126: 1, L0744: 1,
L0747: 1, L0777: 1,
S0242: 1 and S0196: 1. | | |
| 348 | HTADZ74 | 811489 | 358 | 23 - 586 | 971 | Ile-5 to Lys-10,
Arg-78 to Asp-92. | AR050: 18, AR089: 2,
AR061: 2, AR051: 2,
AR054: 1
S0114: 1, H0069: 1,
H0014: 1, L0667: 1,
L0804: 1, L0659: 1,
S0052: 1 and H0422: 1. | | |
| 349 | HAPNZ77 | 887072 | 359 | 1 - 483 | 972 | Lys-82 to Gln-87,
Asp-103 to Ala-108,
Glu-122 to Lys-127. | AR089: 70, AR061:
14, AR050: 9, AR051:
1, AR054: 1 | | |

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|-----|---------|--------|-----|----------|-----|-------------------|--|--|--|
| 350 | HELDR74 | 963001 | 360 | 3 - 1223 | 973 | His-14 to Gln-19. | L0766: 2, H0575: 1,
H0264: 1, L0761: 1 and
L0804: 1.
AR089: 1, AR061: 0
H0305: 4, L0731: 3,
L0581: 3, H0622: 2,
H0059: 2, L0764: 2,
L0766: 2, L0741: 2,
L0740: 2, L0749: 2,
H0423: 2, H0149: 1,
H0159: 1, S0114: 1,
H0656: 1, H0255: 1,
H0306: 1, H0402: 1,
S0045: 1, H0351: 1,
H0550: 1, H0441: 1,
H0036: 1, T0048: 1,
H0318: 1, H0581: 1,
H0024: 1, H0051: 1,
H0083: 1, H0510: 1,
H0617: 1, H0412: 1,
H0280: 1, H0647: 1,
L0646: 1, L0374: 1,
L0385: 1, L0662: 1,
L0767: 1, L0794: 1,
L0649: 1, L0774: 1,
L0806: 1, L0653: 1, | | |
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| 351 | HDPLJ22 | 859915 | 361 | 2 - 547 | 974 | Phe-20 to Lys-37,
Asn-108 to Arg-116. | AR089: 1, AR061: 0
L0591: 20, L0748: 13,
H0090: 5, H0521: 4,
L0758: 4, H0556: 3,
H0656: 3, S0358: 3,
H0038: 3, S0002: 3,
L0794: 3, L0766: 3,
L0803: 3, L0805: 3,
L0791: 3, L0665: 3,
H0547: 3, S0328: 3,
L0747: 3, H0423: 3,
H0624: 2, S0420: 2,
S0046: 2, H0427: 2,
H0156: 2, H0046: 2,
L0471: 2, H0510: 2,
H0424: 2, H0181: 2,
H0264: 2, H0100: 2,
S0426: 2, L0631: 2, | L0657: 1, L0659: 1,
L0783: 1, S0126: 1,
H0690: 1, H0670: 1,
H0672: 1, S0328: 1,
S0380: 1, H0555: 1,
L0748: 1, L0752: 1,
L0758: 1, S0194: 1,
H0542: 1 and H0422: 1. | | |
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| | | | | | | | | | L0771: 1, L0773: 1,
L0650: 1, L0776: 1,
L0655: 1, L0606: 1,
L0629: 1, L0659: 1,
L0809: 1, L0792: 1,
L0666: 1, H0520: 1,
H0593: 1, H0689: 1,
H0659: 1, S0330: 1,
H0522: 1, H0627: 1,
L0742: 1, L0439: 1,
L0740: 1, L0749: 1,
L0779: 1, L0752: 1,
L0757: 1, L0759: 1,
H0445: 1, L0485: 1,
H0653: 1, S0196: 1,
H0542: 1 and H0506: 1. | | | |
| 352 | HPMLD11 | 890204 | 362 | 562 - 2 | 975 | Gln-11 to Trp-22,
Arg-27 to Gly-32,
Pro-47 to Gly-53. | AR054: 115, AR050:
108, AR051: 87,
AR061: 4, AR089: 2
H0644: 3, S0408: 1,
S0280: 1, H0620: 1,
S0364: 1, L0637: 1,
L0764: 1, S0044: 1,
L0611: 1, L0777: 1,
L0755: 1, L0731: 1 and
S0194: 1. | | | | | |

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AR089: 2, AR061: 2,
L0659: 8, L0666: 8,
L0751: 7, L0665: 6,
L0528: 5, L0743: 5,
L0663: 4, H0052: 3,
L0638: 3, L0646: 3,
L0764: 3, L0662: 3,
L0774: 3, L0747: 3,
H0668: 3, S0192: 3,
H0150: 2, H0620: 2,
H0413: 2, H0649: 2,
S0426: 2, L0763: 2,
L0769: 2, L0648: 2,
L0766: 2, L0653: 2,
L0657: 2, S0126: 2,
H0670: 2, L0754: 2,
L0749: 2, H0685: 1,
S0040: 1, H0650: 1,
S0212: 1, H0255: 1,
S0420: 1, S0045: 1,
H0261: 1, H0391: 1,
L0022: 1, H0581: 1,
H0597: 1, H0544: 1,
H0545: 1, H0123: 1,
H0012: 1, H0024: 1,
H0188: 1, S0250: 1,

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| 356 | HHFGZ38 | 785591 | 366 | 302 - 1165 | 979 | | | | H0663: 2, S0328: 2,
S0420: 1, S0046: 1,
H0559: 1, T0082: 1,
H0050: 1, H0100: 1,
H0494: 1, L0640: 1,
L0789: 1, H0436: 1 and
L0439: 1. | | |
| 357 | HDPLN70 | 854010 | 367 | 40 - 828 | 980 | Pro-1 to Gly-7,
Arg-15 to Trp-21,
Pro-58 to Asn-63,
Arg-82 to Gly-88. | | | AR089: 8, AR061: 2
H0556: 1, S0040: 1,
H0657: 1, H0306: 1,
H0393: 1, H0050: 1,
H0266: 1, H0112: 1,
H0063: 1, S0142: 1,
S0002: 1, L0794: 1,
L0378: 1, L0655: 1,
L0791: 1, L0665: 1,
H0539: 1, H0521: 1,
L0596: 1, L0593: 1,
L0595: 1 and H0653: 1.
AR089: 2, AR061: 1
L0766: 26, L0439: 11,
L0757: 8, H0521: 5,
L0748: 5, H0462: 4,
L0745: 4, L0777: 4,
H0013: 3, H0123: 3,
L0774: 3, H0522: 3, | | |

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| 362 | HDQGV77 | 937546 | 372 | 12 - 1379 | 985 | Gln-24 to Gly-30,
Asp-57 to Lys-62,
Leu-109 to Thr-115,
Asn-153 to Gln-166,
Gly-168 to Glu-173,
Gln-184 to Ala-199,
Gly-221 to Pro-232,
Pro-234 to Pro-243, | AR089: 4, AR061: 2
H0521: 17, S0007: 11,
L0747: 11, H0543: 8,
S0278: 7, H0581: 7,
S0344: 7, L0766: 7,
L0745: 7, H0556: 6,
L0769: 6, L0748: 6,
L0731: 6, L0601: 6, | AR089: 4, AR061: 2
H0521: 17, S0007: 11,
L0747: 11, H0543: 8,
S0278: 7, H0581: 7,
S0344: 7, L0766: 7,
L0745: 7, H0556: 6,
L0769: 6, L0748: 6,
L0731: 6, L0601: 6, | T0110: 1, H0123: 1,
H0615: 1, H0033: 1,
H0553: 1, H0212: 1,
H0124: 1, H0040: 1,
H0616: 1, H0264: 1,
H0488: 1, H0100: 1,
H0494: 1, H0131: 1,
H0529: 1, L0637: 1,
L0772: 1, L0766: 1,
L0775: 1, L0375: 1,
L0776: 1, L0628: 1,
L0657: 1, L0664: 1,
S0374: 1, H0547: 1,
H0593: 1, S3014: 1,
S0027: 1, L0748: 1,
L0750: 1, L0731: 1,
L0758: 1, H0595: 1,
S0276: 1 and H0423: 1. |
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| Gln-251 to Ser-259,
Arg-273 to Gly-302,
Lys-317 to Thr-349,
Ala-351 to Arg-368. | H0584: 5, L0157: 5,
H0424: 5, L0758: 5,
H0542: 5, S0049: 4,
H0150: 4, H0050: 4,
H0135: 4, L0666: 4,
H0522: 4, H0436: 4,
L0439: 4, L0750: 4,
H0423: 4, T0002: 3,
H0656: 3, S0001: 3,
H0619: 3, H0617: 3,
T0042: 3, S0142: 3,
S0002: 3, L0770: 3,
L0761: 3, L0378: 3,
L0659: 3, L0665: 3,
H0422: 3, H0171: 2,
H0650: 2, L0005: 2,
H0645: 2, H0455: 2,
H0156: 2, H0575: 2,
H0309: 2, H0457: 2,
H0178: 2, H0620: 2,
T0010: 2, H0083: 2,
S6028: 2, T0006: 2,
H0604: 2, H0180: 2,
H0598: 2, H0090: 2,
H0264: 2, L0775: 2,
L0375: 2, L0655: 2, |
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H0697: 2, H0658: 2,
S0027: 2, L0740: 2,
L0756: 2, L0759: 2,
H0445: 2, L0589: 2,
L0599: 2, H0170: 1,
H0265: 1, H0295: 1,
H0583: 1, H0341: 1,
H0255: 1, H0459: 1,
H0638: 1, H0637: 1,
S0045: 1, S6026: 1,
H0351: 1, S6016: 1,
S0222: 1, H0392: 1,
H0574: 1, H0486: 1,
H0013: 1, H0250: 1,
H0069: 1, H0075: 1,
H0427: 1, H0042: 1,
H0036: 1, H0004: 1,
S0010: 1, T0048: 1,
H0318: 1, H0434: 1,
H0052: 1, H0086: 1,
H0572: 1, H0123: 1,
H0012: 1, H0024: 1,
S0051: 1, H0594: 1,
H0428: 1, H0031: 1,
H0165: 1, L0456: 1, |
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H0616: 1, H0063: 1,
H0551: 1, H0488: 1,
S0038: 1, H0130: 1,
H0695: 1, L0520: 1,
L0640: 1, L0667: 1,
L0772: 1, L0764: 1,
L0771: 1, L0662: 1,
L0363: 1, L0767: 1,
L0768: 1, L0803: 1,
L0804: 1, L0650: 1,
L0805: 1, L0809: 1,
H0144: 1, S0310: 1,
L0438: 1, L0352: 1,
H0660: 1, H0648: 1,
H0672: 1, S0330: 1,
H0518: 1, H0696: 1,
H0187: 1, S3014: 1,
S0028: 1, S0032: 1,
L0743: 1, L0754: 1,
L0746: 1, L0749: 1,
L0779: 1, H0343: 1,
H0595: 1, L0591: 1,
L0592: 1, L0608: 1,
L0595: 1, L0366: 1,
S0106: 1 and H0352: 1. | | |
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| 363 | HE8TM80 | 955022 | 373 | 358 - 696 | 986 | Arg-1 to Asn-7,
Leu-56 to Met-61. | AR089: 9, AR061: 7
H0040: 5, H0547: 5,
S0152: 5, L0593: 5,
L0595: 5, H0551: 4,
H0529: 4, H0519: 4,
H0560: 3, H0561: 3,
H0657: 2, S0360: 2,
S0007: 2, H0586: 2,
H0013: 2, H0494: 2,
L0809: 2, H0435: 2,
S0028: 2, L0748: 2,
L0439: 2, L0731: 2,
L0759: 2, H0445: 2,
L0592: 2, H0542: 2,
H0624: 1, H0170: 1,
H0556: 1, S0212: 1,
H0663: 1, S0418: 1,
S0356: 1, S0046: 1,
H0393: 1, H0486: 1,
H0427: 1, H0156: 1,
H0036: 1, H0318: 1,
T0110: 1, H0545: 1,
H0014: 1, H0266: 1,
H0188: 1, S0022: 1,
H0328: 1, H0688: 1,
T0023: 1, H0032: 1, | | |
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| 364 | HWLEY40 | 957875 | 374 | 3 - 881 | 987 | Glu-6 to Gly-11,
Gly-64 to Ser-70,
Val-140 to Val-145,
His-163 to Leu-168,
Leu-189 to Lys-198,
Ser-221 to Thr-227,
His-261 to Pro-270. | AR089: 2, AR061: 2
L0438: 12, L0439: 11,
H0617: 5, H0556: 4,
H0618: 3, H0253: 3,
L0769: 3, L0761: 3,
L0759: 3, H0544: 2,
H0031: 2, H0135: 2,
H0038: 2, H0641: 2,
L0764: 2, L0783: 2, | | |
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L0809: 2, L0790: 2,
L0666: 2, L0663: 2,
L0665: 2, H0144: 2,
S0330: 2, L0751: 2,
L0779: 2, H0543: 2,
H0265: 1, H0685: 1,
H0657: 1, H0306: 1
S0420: 1, S0354: 1,
S0360: 1, S0046: 1,
L0717: 1, H0550: 1,
H0592: 1, H0333: 1,
H0331: 1, H0559: 1,
H0486: 1, H0013: 1,
H0244: 1, H0635: 1,
H0575: 1, H0596: 1,
T0110: 1, H0123: 1,
H0615: 1, H0033: 1,
H0553: 1, H0212: 1,
H0124: 1, H0040: 1,
H0616: 1, H0264: 1,
H0488: 1, H0100: 1,
H0494: 1, H0131: 1,
H0529: 1, L0637: 1,
L0772: 1, L0766: 1,
L0775: 1, L0375: 1,
L0776: 1, L0628: 1,

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|-----|---------|--------|-----|----------|-----|---|---|--|--|---|
| 367 | HMIAH32 | 550977 | 377 | 49 - 702 | 990 | His-15 to Ser-21,
Asp-44 to Val-65,
Glu-95 to Thr-101,
Ala-131 to Asp-142. | AR061: 7, AR089: 2
S6028: 2, L0766: 2,
L0777: 2, L0752: 2,
H0663: 1, H0696: 1 and
L0779: 1. | | | 601238,
601846,
602216,
602477 |
| 368 | HDPTH43 | 573418 | 378 | 1 - 432 | 991 | Ser-28 to Glu-34,
Ser-77 to Arg-82,
Trp-127 to Arg-135. | AR061: 2, AR089: 1
S0116: 2, H0586: 1 and
H0521: 1. | | | |
| 369 | HCE3W04 | 615501 | 379 | 94 - 873 | 992 | | AR089: 1, AR061: 0
L0789: 4, L0731: 4,
H0539: 3, L0779: 3,
S0007: 2, H0052: 2,
L0157: 2, H0123: 2,
H0233: 2, L0637: 2,
S0356: 1, S0360: 1,
H0550: 1, H0253: 1,
H0620: 1, H0408: 1,
H0188: 1, S0250: 1,
L0193: 1, L0455: 1,
H0135: 1, H0551: 1,
L0770: 1, L0794: 1,
L0776: 1, L0665: 1, | | | |

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|-----|---------|--------|-----|-----------|-----|---|---|------|--|
| 370 | HMUBZ20 | 670393 | 380 | 2 - 184 | 993 | Gly-42 to Ser-48. | S0392: 1, L0750: 1 and L0777: 1.
AR089: 13, AR061: 3
H0529: 1 and H0693: 1. | 5q23 | 121050,
126150,
159000,
179095,
192974,
192974,
601596 |
| 371 | HDPAB51 | 685665 | 381 | 288 - 953 | 994 | Ser-18 to Ile-27,
Asp-124 to Gln-138. | AR089: 2, AR061: 2
H0521: 2, L0759: 2,
H0341: 1, H0620: 1,
H0266: 1 and L0766: 1. | | |
| 372 | HPJAP28 | 686349 | 382 | 2 - 415 | 995 | Pro-25 to Ala-34,
Ser-69 to Ala-74,
Glu-92 to Gly-98. | AR061: 6, AR089: 3
H0622: 2, H0253: 1
and S0152: 1. | | |
| 373 | HIBEC79 | 703000 | 383 | 338 - 3 | 996 | Ser-7 to Asp-13. | AR089: 1, AR061: 0
L0766: 5, L0806: 3,
T0010: 2, L0761: 2,
H0521: 2, L0752: 2,
H0677: 2, S0278: 1,
H0559: 1, H0486: 1,
H0427: 1, S0038: 1,
L0796: 1, L0644: 1,
L0771: 1, L0659: 1,
L0666: 1, L0664: 1, | | |

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|-----|---------|--------|-----|-----------|-----|-------------------|---|-----------|---|
| 374 | HOQBF64 | 703177 | 384 | 48 - 401 | 997 | | L0779: 1, H0445: 1 and
L0595: 1.
AR089: 23, AR061: 14
H0208: 1 and H0290:
1. | 17q23-q24 | 106180,
115660,
138700,
139250,
148500,
150200,
154275,
162100,
170500,
170500,
170500,
176960,
182452,
230200,
249000,
253250 |
| 375 | HTEDL38 | 761609 | 385 | 133 - 534 | 998 | Pro-38 to Pro-46. | AR061: 3, AR089: 2
H0038: 4, L0748: 4,
S0222: 2, L0598: 2,
L0776: 2, L0439: 2,
L0780: 2, L0752: 2,
H0050: 1, T0006: 1,
H0111: 1, S0036: 1,
H0616: 1, T0067: 1, | | |

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|-----|----------|--------|-----|-----------|------|--|--|--|--|--|
| | | | | | | | | S0038: 1, L0770: 1,
L0766: 1, L0774: 1,
L0805: 1, L0655: 1,
L0526: 1, L0666: 1,
L0438: 1, S0028: 1,
L0777: 1, L0595: 1 and
L0366: 1. | | |
| 376 | HE9HI71 | 779375 | 386 | 2 - 682 | 999 | | | AR089: 1, AR061: 1
H0013: 3, T0010: 1,
L0435: 1, H0144: 1,
L0438: 1 and L0439: 1. | | |
| 377 | HNFFHS82 | 779946 | 387 | 2 - 415 | 1000 | | | AR061: 4, AR089: 2
S0278: 1, H0620: 1 and
H0271: 1. | | |
| 378 | HOUHO89 | 786548 | 388 | 367 - 909 | 1001 | Ser-1 to Gly-7,
Asp-24 to Leu-31,
Lys-50 to Arg-58,
Glu-65 to Arg-73,
Thr-102 to His-109,
Arg-116 to Ile-122. | | AR089: 1, AR061: 1
S0342: 1 and H0521: 1. | | |
| 379 | HFPBB28 | 844526 | 389 | 3 - 335 | 1002 | Ala-11 to Gln-16,
Leu-46 to Ala-52,
Gln-84 to Glu-89,
Phe-105 to Ser-111. | | AR054: 10, AR051: 2,
AR050: 2, AR061: 1,
AR089: 0
S0031: 2, S0001: 1,
S0045: 1, S0222: 1,
H0271: 1, S0144: 1, | | |

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|-----|---------|--------|-----|----------|------|--|---|--|--|
| 383 | HSLIH01 | 884251 | 393 | t1 - 649 | 1006 | <p>Arg-14 to Glu-20,
Leu-30 to Arg-42,
Gly-57 to Ala-65,
Asn-99 to Arg-104,
Asn-111 to Ser-117.</p> | <p>AR089: 3, AR061: 2,
AR051: 2, AR050: 1,
AR054: 1
L0775: 4, H0046: 3,
H0622: 3, H0660: 3,
H0402: 2, H0438: 2,
L0663: 2, L0665: 2,
L0777: 2, S0026: 2,</p> | | |
| | | | | | | <p>Phe-107 to Gly-112,
Arg-125 to Glu-131,
Leu-141 to Arg-153,
Gly-168 to Ala-176,
Asn-210 to Arg-215,
Asn-222 to Ser-234,
Leu-238 to Thr-249.</p> | <p>H0438: 2, L0663: 2,
L0665: 2, L0777: 2,
S0026: 2, H0583: 1,
S0282: 1, S0356: 1,
H0051: 1, H0071: 1,
H0355: 1, H0510: 1,
H0615: 1, H0428: 1,
H0644: 1, L0142: 1,
S0364: 1, H0059: 1,
L0763: 1, L0803: 1,
L0804: 1, L0657: 1,
L0809: 1, L0664: 1,
H0690: 1, H0670: 1,
H0672: 1, H0479: 1,
S0028: 1, L0751: 1,
S0031: 1, L0604: 1,
L0366: 1, S0192: 1 and
S0424: 1.</p> | | |

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|-----|---------|--------|-----|------------|------|--|--|--|--|--|--|---|--|--|--|
| | | | | | | | | | | | | H0583: 1, S0282: 1,
S0356: 1, H0051: 1,
H0071: 1, H0355: 1,
H0510: 1, H0615: 1,
H0428: 1, H0644: 1,
L0142: 1, S0364: 1,
H0059: 1, L0763: 1,
L0803: 1, L0804: 1,
L0657: 1, L0809: 1,
L0666: 1, L0664: 1,
H0144: 1, H0690: 1,
H0670: 1, H0672: 1,
H0479: 1, S0028: 1,
L0751: 1, S0031: 1,
L0604: 1, L0366: 1,
S0192: 1 and S0424: 1. | | | |
| 384 | HE9OV91 | 887364 | 394 | 34 - 723 | 1007 | | | | | | | AR054: 2, AR051: 2,
AR050: 1, AR089: 0,
AR061: 0
S0116: 1, H0619: 1,
H0421: 1, H0144: 1,
L0748: 1 and L0758: 1. | | | |
| 385 | HHEDS85 | 894602 | 395 | 2 - 457 | 1008 | Ser-12 to Ser-19,
Ser-34 to Lys-47. | | | | | | AR061: 2, AR089: 1
T0039: 1, H0144: 1
and H0542: 1. | | | |
| 386 | HNTDJ68 | 899624 | 396 | 667 - 1599 | 1009 | Phe-40 to Tyr-47, | | | | | | AR051: 25, AR050: | | | |

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|-----|---------|--------|-----|------------|------|---|--|--|--|
| 390 | HHEMD52 | 909742 | 400 | 623 - 1618 | 1013 | Trp-3 to Thr-14,
Ala-21 to Arg-30,
Glu-66 to Pro-74,
Pro-103 to Gly-108,
Ile-135 to Ile-142. | L0779: 1.
AR089: 4, AR061: 3
H0457: 3, H0271: 3,
H0543: 3, H0422: 2,
H0583: 1, H0650: 1,
H0484: 1, H0483: 1,
S0442: 1, H0580: 1,
S0140: 1, H0486: 1,
H0250: 1, H0050: 1,
H0630: 1, H0264: 1,
H0488: 1, H0487: 1,
S0002: 1, L0439: 1,
H0707: 1, H0136: 1 and
H0677: 1. | | |
| 391 | HSIDQ38 | 909854 | 401 | 3 - 764 | 1014 | Ala-18 to Arg-23,
Gly-28 to Trp-35,
Gln-53 to Arg-61,
Asp-122 to Glu-127,
Gln-163 to Cys-171. | AR061: 3, AR089: 3
L0766: 5, H0587: 2,
H0036: 2, L0745: 2,
L0747: 2, H0556: 1,
S0114: 1, H0590: 1,
H0052: 1, L0640: 1,
L0770: 1, L0771: 1,
L0659: 1 and L0665: 1. | | |
| 392 | HSKBF02 | 909855 | 402 | 3 - 395 | 1015 | Gly-35 to Asp-41. | AR089: 53, AR061: 14
L0438: 6, L0751: 6,
L0439: 5, L0770: 4,
H0052: 2, H0620: 2, | | |

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|-----|---------|--------|-----|----------|------|--|--|---|--|--|--|--|
| 393 | HIBDE74 | 766011 | 403 | 99 - 362 | 1016 | | | | H0521: 2, L0756: 2,
L0731: 2, L0758: 2,
L0588: 2, H0556: 1,
S0282: 1, H0662: 1,
H0402: 1, S0418: 1,
T0008: 1, S0222: 1,
H0392: 1, H0333: 1,
L0021: 1, H0581: 1,
S0049: 1, L0471: 1,
H0266: 1, L0351: 1,
L0772: 1, L0766: 1,
L0776: 1, L0659: 1,
L0792: 1, H0522: 1,
S0027: 1, L0779: 1 and
S0011: 1. | | | |
| | | 909876 | 621 | 2 - 751 | 1234 | | | | AR089: 1, AR061: 1
L0759: 2, H0171: 1,
T0010: 1, H0090: 1,
L0761: 1, L0766: 1,
S3014: 1, L0745: 1,
L0747: 1 and H0506: 1. | | | |
| 394 | HWMAE53 | 909877 | 404 | 1 - 438 | 1017 | | | Glu-7 to Gln-17,
Tyr-27 to Cys-32,
Thr-63 to Lys-70,
Glu-89 to Lys-94, | AR089: 3, AR061: 1
S0354: 1 and H0030: 1. | | | |

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| 398 | HTXJA84 | 911387 | 408 | 2 - 628 | 1021 | Arg-1 to Ser-6,
Asn-55 to Phe-64,
Ser-86 to Gly-92,
Leu-124 to Glu-146. | L0157: 2, H0123: 2,
H0233: 2, L0637: 2,
S0356: 1, S0360: 1,
H0550: 1, H0253: 1,
H0620: 1, H0408: 1,
H0188: 1, S0250: 1,
L0193: 1, L0455: 1,
H0135: 1, H0551: 1,
L0770: 1, L0794: 1,
L0776: 1, L0665: 1,
S0392: 1, L0750: 1 and
L0777: 1. | | |
| 399 | HKAAW89 | 911389 | 409 | 1 - 447 | 1022 | Gln-12 to Pro-20,
Thr-37 to Glu-42,
Ile-49 to Arg-56, | AR061: 5, AR089: 2
H0521: 4, H0457: 3,
H0580: 2, L0749: 2,
L0588: 2, H0556: 1,
H0485: 1, H0635: 1,
H0581: 1, H0251: 1,
H0124: 1, H0551: 1,
H0529: 1, L0667: 1,
L0773: 1, L0803: 1,
S0052: 1, H0593: 1 and
S0424: 1. | | |

HWAF84 911559 412 1-702 1025

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|-----|--------|--------|-----|---------|------|--|--|--|--|--------------------|---------|---|
| 402 | HWAF84 | 911559 | 412 | 1 - 702 | 1025 | | | | H0677: 2, H0556: 1,
H0584: 1, H0140: 1,
H0583: 1, H0656: 1,
H0402: 1, H0305: 1,
H0458: 1, S0140: 1,
H0550: 1, H0497: 1,
H0575: 1, S0474: 1,
H0421: 1, H0024: 1,
H0213: 1, H0087: 1,
H0272: 1, H0641: 1,
S0144: 1, L0763: 1,
L0761: 1, L0662: 1,
L0794: 1, L0803: 1,
L0804: 1, L0659: 1,
L0787: 1, L0666: 1,
L0663: 1, H0518: 1,
S0044: 1, H0576: 1,
L0756: 1, H0422: 1,
S0452: 1 and H0506: 1. | AR061: 2, AR089: 1 | 19p13.3 | 108725,
120700,
133171,
136836,
145981,
147141,
164953, |
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|-----|---------|--------|-----|---------|------|---|--|--|---|
| 403 | HETCL18 | 914535 | 413 | 1 - 684 | 1026 | Lys-12 to Pro-22,
Lys-38 to Thr-45,
Glu-65 to Lys-70,
Phe-78 to Gly-83,
Arg-96 to Glu-102,
Leu-112 to Arg-124,
Gly-139 to Ala-147,
Asn-181 to Arg-186,
Asn-193 to Ser-205,
Leu-209 to Thr-220. | AR054: 8, AR061: 5,
AR089: 5, AR050: 1,
AR051: 1
L0754: 45, L0747: 8,
H0553: 7, L0775: 5,
L0755: 5, L0659: 4,
H0046: 3, H0622: 3,
H0124: 3, L0665: 3,
H0660: 3, L0748: 3,
L0751: 3, H0402: 2,
H0438: 2, H0586: 2,
H0427: 2, H0599: 2,
H0575: 2, H0050: 2,
L0471: 2, H0644: 2,
H0616: 2, H0056: 2,
L0764: 2, L0662: 2,
L0794: 2, L0803: 2,
L0804: 2, L0666: 2,
L0663: 2, H0144: 2,
L0749: 2, L0750: 2, | | 188070,
600957,
601238,
601846,
602216,
602477 |
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| | | | | | L0777: 2, S0026: 2,
H0583: 1, S0282: 1,
H0305: 1, S0356: 1,
S0358: 1, S0045: 1,
S0046: 1, H0619: 1,
H0485: 1, S0280: 1,
H0042: 1, H0569: 1,
H0024: 1, H0051: 1,
H0071: 1, H0355: 1,
H0510: 1, H0328: 1,
H0615: 1, H0428: 1,
H0030: 1, L0142: 1,
S0364: 1, H0361: 1,
H0040: 1, H0413: 1,
H0059: 1, S0038: 1,
L0763: 1, L0770: 1,
L0769: 1, L0800: 1,
L0644: 1, L0363: 1,
L0806: 1, L0657: 1,
L0783: 1, L0809: 1,
L0664: 1, H0519: 1,
H0690: 1, H0670: 1,
H0672: 1, S0146: 1,
H0555: 1, H0479: 1,
S3012: 1, S0028: 1,
L0779: 1, L0731: 1, | | | | |
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| 404 | HCRNK75 | 914536 | 414 | 2156 - 912 | 1027 | Pro-1 to Met-7,
Ala-16 to Gly-24,
Gly-26 to Leu-33,
Lys-57 to Pro-67,
Lys-83 to Thr-90,
Glu-110 to Lys-115,
Phe-123 to Gly-128,
Arg-141 to Glu-147,
Leu-157 to Arg-169,
Gly-184 to Ala-192,
Asn-226 to Arg-231,
Asn-238 to Ser-250,
Leu-254 to Thr-265. | S0031: 1, L0605: 1,
L0599: 1, L0604: 1,
L0603: 1, L0366: 1,
S0192: 1, H0543: 1,
S0424: 1 and H0506: 1.
AR061: 124, AR089:
76
L0775: 4, H0046: 3,
H0622: 3, H0660: 3,
H0438: 2, L0663: 2,
L0665: 2, L0777: 2,
S0026: 2, H0583: 1,
S0282: 1, S0356: 1,
H0051: 1, H0071: 1,
H0355: 1, H0510: 1,
H0615: 1, H0428: 1,
H0644: 1, L0142: 1,
S0364: 1, H0059: 1,
L0763: 1, L0803: 1,
L0804: 1, L0657: 1,
L0809: 1, L0664: 1,
H0690: 1, H0670: 1,
H0672: 1, H0479: 1,
S0028: 1, L0751: 1,
S0031: 1, L0604: 1,
L0366: 1, S0192: 1 and | | |
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HTPFA03 922765 415 2 - 328 1028 S0424: 1, AR061: 4, AR089: 2, H0622: 2, S0212: 1, H0253: 1, S0152: 1, L0748: 1, L0603: 1 and H0668: 1.

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|-----|---------|--------|-----|----------|------|--|--|--|--|--|--|
| 405 | HTPFA03 | 922765 | 415 | 2 - 328 | 1028 | | | | S0424: 1, AR061: 4, AR089: 2, H0622: 2, S0212: 1, H0253: 1, S0152: 1, L0748: 1, L0603: 1 and H0668: 1. | | |
| 406 | HWADR60 | 926487 | 416 | 3 - 1289 | 1029 | Gln-15 to Asp-21, Leu-40 to Asp-47, Gly-70 to Leu-84, Leu-88 to Arg-93, Lys-98 to Asp-105, Glu-136 to Arg-148, Thr-197 to Ala-204, Asp-222 to Glu-232, Glu-261 to Gln-269, Arg-295 to Trp-300, Asn-306 to Pro-314, Lys-395 to Lys-415. | | | AR089: 104, AR061: 11, S0278: 4, H0581: 4, L0751: 4, H0620: 3, L0764: 3, L0662: 3, L0659: 3, L0439: 3, L0754: 3, H0542: 3, H0170: 2, H0402: 2, H0580: 2, H0550: 2, H0333: 2, H0012: 2, T0010: 2, H0252: 2, H0063: 2, H0059: 2, S0002: 2, L0775: 2, L0655: 2, L0663: 2, L0665: 2, H0593: 2, H0658: 2, H0539: 2, H0555: 2, L0743: 2, L0744: 2, L0752: 2, L0731: 2, H0543: 2, H0624: 1, H0265: 1, | | |

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| | | H0650: 1, H0656: 1,
S0212: 1, H0306: 1,
H0305: 1, S0360: 1,
S0046: 1, H0619: 1,
S0222: 1, S6014: 1,
H0613: 1, H0492: 1,
H0250: 1, H0635: 1,
H0427: 1, L0021: 1,
H0036: 1, H0421: 1,
H0399: 1, H0416: 1,
H0188: 1, S0250: 1,
L0143: 1, H0617: 1,
H0673: 1, H0124: 1,
H0163: 1, H0634: 1,
H0087: 1, T0067: 1,
H0264: 1, H0272: 1,
H0412: 1, H0413: 1,
H0100: 1, S0344: 1,
S0426: 1, L0770: 1,
L0638: 1, L0761: 1,
L0794: 1, L0650: 1,
L0661: 1, L0546: 1,
S0053: 1, H0689: 1,
H0521: 1, S3014: 1,
L0748: 1, L0740: 1,
L0779: 1, L0780: 1, | | | | |
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| 407 | HWLFJ01 | 928017 | 417 | 1 - 780 | 1030 | Arg-11 to Arg-19,
Ser-36 to Thr-61,
Glu-79 to Glu-84,
Ala-100 to Gln-106,
Ser-155 to Leu-161. | L0753: 1, L0759: 1,
H0445: 1, H0595: 1,
L0362: 1, H0653: 1 and
H0506: 1.

AR061: 3, AR089: 2
L0741: 12, L0744: 6,
H0052: 5, H0040: 5,
L0742: 5, L0748: 5,
H0620: 4, L0794: 4,
H0486: 3, H0622: 3,
L0439: 3, L0749: 3,
L0777: 3, S0354: 2,
H0046: 2, H0031: 2,
H0617: 2, L0770: 2,
L0761: 2, L0806: 2,
S0126: 2, H0539: 2,
H0518: 2, H0521: 2,
L0751: 2, L0747: 2,
L0758: 2, L0593: 2,
H0624: 1, H0171: 1,
S0114: 1, H0650: 1,
S0418: 1, S0420: 1,
H0645: 1, H0351: 1,
H0370: 1, H0600: 1,
H0592: 1, L0622: 1,
T0082: 1, S0474: 1. | | |
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|-----|---------|--------|-----|----------|------|---|--|--|--|
| 409 | HPCIG66 | 930886 | 419 | 30 - 653 | 1032 | Asn-48 to Gly-54,
Thr-56 to Lys-69. | H0632: 1, H0618: 1,
H0271: 1, S0368: 1,
H0673: 1, L0667: 1,
L0662: 1, L0767: 1,
L0768: 1, L0381: 1,
L0789: 1, L0790: 1,
L0664: 1, L0665: 1,
H0659: 1, H0658: 1,
S0328: 1, S0454: 1,
L0749: 1, L0777: 1,
H0542: 1 and H0677: 1. | | |
| 410 | HCRPU72 | 931140 | 420 | 2 - 799 | 1033 | Gly-1 to Val-11,
Gly-50 to Thr-62,
Asn-125 to Gly-132,
Leu-172 to Asn-178,
Ser-210 to Ser-217,
Ser-232 to Lys-245. | AR089: 16, AR061: 6
H0144: 6, H0013: 2
and S0356: 1. | | |
| 411 | HE9RT95 | 934556 | 421 | 1 - 714 | 1034 | Leu-21 to Asp-33. | AR089: 17, AR061: 13
S0049: 1, H0144: 1 and
L0439: 1. | | |
| 412 | HFXJM13 | 935725 | 422 | 16 - 438 | 1035 | Gln-36 to Thr-42,
Glu-99 to Leu-104. | AR061: 1, AR089: 0
L0748: 7, L0766: 6,
L0756: 5, H0580: 4,
L0777: 3, H0052: 2 | | |

| | | | | | | | | | | | | |
|-----|---------|--------|-----|----------|------|--|---|---------|--|--|--|--|
| | | | | | | | | | L0792: 1, L0663: 1,
L0438: 1, H0547: 1,
S0126: 1, L0439: 1,
L0740: 1, L0749: 1,
L0752: 1, S0031: 1,
H0445: 1, L0480: 1,
L0604: 1, S0026: 1,
H0542: 1, S0412: 1 and
H0352: 1. | | | |
| 413 | HDPWU37 | 940705 | 423 | 3 - 536 | 1036 | Glu-8 to Pro-17,
Pro-31 to Asp-37. | AR089: 12, AR061: 6
H0575: 1, H0271: 1
and H0521: 1. | 22q13.1 | 103050,
103050,
124030,
124030,
138981,
182380,
188826,
190040,
190040,
190040 | | | |
| 414 | HHSDL85 | 942246 | 424 | 2 - 502 | 1037 | Ser-12 to Gln-25,
Pro-29 to Phe-39,
Gly-81 to Gly-89,
Glu-143 to Trp-156. | AR061: 3, AR089: 2
S0007: 3, S0001: 1,
H0618: 1, H0009: 1,
S0051: 1, L0763: 1,
L0439: 1 and L0758: 1. | | | | | |
| | | 951168 | 622 | 356 - 42 | 1235 | Arg-82 to Trp-88. | | | | | | |
| 415 | HTJMD31 | 942848 | 425 | 1 - 462 | 1038 | Pro-17 to Asn-23. | AR089: 14, AR061: 6 | | | | | |

| | | | | | | | | | |
|-----|---------|--------|-----|------------|------|---|---|--|--|
| 416 | HWADD57 | 943039 | 426 | 2 - 1009 | 1039 | Asp-2 to Pro-7,
Leu-18 to Arg-27,
Glu-52 to Ser-59,
Pro-90 to Pro-97,
Pro-116 to Glu-121. | S0300: 2, L0439: 2,
H0438: 1, H0618: 1,
H0052: 1, H0616: 1,
H0488: 1, L0772: 1,
L0806: 1, L0384: 1,
L0666: 1, L0758: 1 and
H0423: 1. | | |
| 417 | HLWAH05 | 944904 | 427 | 356 - 1351 | 1040 | Ala-1 to Arg-9,
Leu-11 to Pro-18. | AR061: 2, AR089: 1
H0586: 5, L0751: 2,
H0170: 1, H0638: 1,
H0553: 1, H0477: 1,
S0002: 1, H0529: 1,
L0766: 1, L0803: 1,
H0672: 1 and H0543: 1. | | |
| 418 | HDPCI84 | 945527 | 428 | 25 - 1047 | 1041 | Arg-9 to Arg-18,
Leu-107 to Gln-113,
Asp-126 to Thr-131. | AR089: 2, AR061: 1
H0521: 4, L0803: 3,
S0358: 2, H0489: 2,
H0046: 2, L0794: 2,
L0666: 2, H0144: 2,
S0126: 2, S0342: 1,
H0663: 1, S0356: 1, | | |

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|-----|---------|--------|-----|---------|------|--|---|--|--|
| 420 | HAMFD12 | 952438 | 430 | 3 - 539 | 1043 | Tyr-41 to Leu-52,
Leu-64 to Cys-72,
Pro-92 to Arg-98,
Ser-110 to Glu-116. | L0789: 1, H0144: 1,
L0745: 1 and L0746: 1.
AR089: 3, AR061: 1
H0271: 10, H0052: 8,
H0556: 7, L0439: 7,
L0754: 7, H0622: 6,
L0776: 5, L0769: 4,
H0265: 3, H0295: 3,
H0580: 3, S0222: 3,
H0013: 3, H0156: 3,
H0051: 3, H0494: 3,
L0659: 3, S0356: 2,
H0208: 2, S6014: 2,
H0135: 2, H0634: 2,
S0002: 2, S0426: 2,
L0770: 2, L0796: 2,
L0373: 2, L0803: 2,
L0375: 2, L0655: 2,
L0666: 2, L0438: 2,
H0672: 2, H0521: 2,
L0747: 2, L0750: 2,
L0756: 2, L0588: 2,
H0542: 2, H0543: 2,
H0170: 1, S0212: 1,
S0282: 1, S0030: 1,
H0305: 1, H0589: 1, | | |
|-----|---------|--------|-----|---------|------|--|---|--|--|

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|--|--|--|--|--|--|--|
| | | | | | L0619: 1, H0619: 1,
S6026: 1, H0550: 1,
H0370: 1, H0600: 1,
H0592: 1, H0486: 1,
T0040: 1, H0635: 1,
H0002: 1, S0010: 1,
H0390: 1, H0581: 1,
H0421: 1, H0085: 1,
T0110: 1, H0041: 1,
N0006: 1, H0050: 1,
H0012: 1, H0620: 1,
T0003: 1, H0024: 1,
H0687: 1, H0252: 1,
H0604: 1, H0031: 1,
H0644: 1, H0628: 1,
H0598: 1, H0087: 1,
H0264: 1, S0112: 1,
T0041: 1, H0560: 1,
S0150: 1, H0529: 1,
L0640: 1, L0761: 1,
L0643: 1, L0806: 1,
L0658: 1, L0809: 1,
L0544: 1, L0788: 1,
L0663: 1, L0664: 1,
L0665: 1, S0428: 1,
S0053: 1, H0144: 1, | |
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|-----|---------|--------|-----|------------|------|-------------------|--|--|---|--|--|--|
| | | | | | | | | | S0136: 3, L0779: 3,
H0171: 1, H0052: 1,
H0038: 1, L0766: 1,
H0547: 1, S0031: 1 and
S0242: 1. | | | |
| 425 | HWLHF10 | 963422 | 435 | 115 - 978 | 1048 | Ile-44 to Gln-50. | | | AR089: 26, AR061: 4
S0354: 1, H0561: 1 and
L0603: 1. | | | |
| 426 | HOEMG82 | 963855 | 436 | 2 - 991 | 1049 | Asp-1 to Pro-12. | | | AR061: 49, AR089: 19 | | | |
| 427 | HFXDR37 | 965915 | 437 | 1485 - 556 | 1050 | Glu-18 to Thr-23. | | | AR061: 2, AR089: 1
L0766: 2, S0001: 1,
H0592: 1, H0575: 1,
H0644: 1, H0038: 1 and
H0144: 1. | | | |
| 428 | HNNAS46 | 969470 | 438 | 1 - 834 | 1051 | | | | AR089: 1, AR061: 0
H0638: 2, H0521: 2,
L0752: 2, H0677: 2,
H0650: 1, H0484: 1,
H0458: 1, H0580: 1,
H0586: 1, H0575: 1,
H0081: 1, S0036: 1,
H0063: 1, H0560: 1,
L0809: 1, S0126: 1,
S0328: 1, L0744: 1,
L0740: 1, L0754: 1 and | | | |

| | | | | | | | | | | |
|-----|---------|--------|-----|------------|------|--------------------------------------|--|---|--|--|
| 431 | HCETF22 | 973324 | 441 | 112 - 1863 | 1054 | Asn-1 to Gly-9,
Gln-30 to Glu-35. | AR061: 11, AR089: 4
L0741: 8, L0766: 7,
L0794: 6, H0306: 4,
H0052: 4, L0768: 3,
L0803: 3, H0542: 3,
S0360: 2, H0457: 2,
H0617: 2, H0606: 2,
S0036: 2, H0100: 2,
L0800: 2, H0672: 2,
H0436: 2, L0777: 2,
H0543: 2, H0650: 1,
L0785: 1, H0341: 1,
H0254: 1, H0402: 1,
S0420: 1, H0580: 1,
S0045: 1, H0645: 1,
H0550: 1, S0222: 1, | S0374: 1, H0435: 1,
H0670: 1, H0651: 1,
H0521: 1, H0436: 1,
H0345: 1, L0439: 1,
L0745: 1, L0749: 1,
L0750: 1, L0759: 1,
L0485: 1, L0593: 1,
S0026: 1, H0665: 1,
H0543: 1, H0423: 1,
H0422: 1 and S0458: 1. | | |
|-----|---------|--------|-----|------------|------|--------------------------------------|--|---|--|--|

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|-----|---------|--------|-----|-----------|------|---|--|--|--|
| 432 | HCMSF55 | 912284 | 442 | 657 - 361 | 1055 | <p>S6014: 1, H0592: 1,
N0009: 1, S0280: 1,
H0599: 1, H0618: 1,
S0182: 1, H0581: 1,
S0049: 1, H0194: 1,
N0007: 1, H0271: 1,
H0252: 1, H0063: 1,
H0488: 1, H0412: 1,
H0079: 1, T0041: 1,
H0646: 1, S0144: 1,
L0763: 1, L0770: 1,
L0769: 1, L0761: 1,
L0372: 1, L0646: 1,
L0645: 1, L0764: 1,
L0774: 1, L0792: 1,
L0666: 1, L0665: 1,
H0519: 1, H0435: 1,
H0539: 1, H0518: 1,
L0747: 1, L0755: 1,
H0653: 1, H0136: 1,
H0677: 1 and S0446: 1.</p> | <p>AR089: 2, AR061: 2
L0604: 16, S0366: 9,
L0485: 7, L0622: 6,
L0623: 6, H0599: 6,
H0373: 6, H0196: 4,</p> | | |
|-----|---------|--------|-----|-----------|------|---|--|--|--|

| | | | | | | | |
|--------|-----|----------|------|--|--|---|--|
| | | | | | | L0163: 4, L0777: 4,
L0520: 3, H0002: 2,
S0364: 2, S0330: 2,
L0747: 2, H0171: 1,
H0549: 1, H0486: 1,
H0013: 1, H0253: 1,
H0318: 1, S0049: 1,
H0251: 1, L0471: 1,
S0051: 1, H0616: 1,
S0038: 1, H0100: 1,
H0561: 1, L0803: 1,
L0782: 1, L0809: 1,
L0779: 1, L0759: 1 and
L0584: 1. | |
| 975280 | 623 | 52 - 705 | 1236 | His-10 to Gly-16,
Pro-65 to Ala-70,
Ala-96 to Lys-101. | | | |

[51] The first column in Table 1A provides the gene number in the application corresponding to the clone identifier. The second column in Table 1A provides a unique "Clone ID NO:Z" for a cDNA clone related to each contig sequence disclosed in Table 1A. This clone ID references the cDNA clone which contains at least the 5' most sequence of the assembled contig and at least a portion of SEQ ID NO:X was determined by directly sequencing the referenced clone. The reference clone may have more sequence than described in the sequence listing or the clone may have less. In the vast majority of cases, however, the clone is believed to encode a full-length polypeptide. In the case where a clone is not full-length, a full-length cDNA can be obtained by methods described elsewhere herein.

[52] The third column in Table 1A provides a unique "Contig ID" identification for each contig sequence. The fourth column provides the "SEQ ID NO:" identifier for each of the contig polynucleotide sequences disclosed in Table 1A. The fifth column, "ORF (From-To)", provides the location (i.e., nucleotide position numbers) within the polynucleotide sequence "SEQ ID NO:X" that delineate the preferred open reading frame (ORF) shown in the sequence listing and referenced in Table 1A, column 6, as SEQ ID NO:Y. Where the nucleotide position number "To" is lower than the nucleotide position number "From", the preferred ORF is the reverse complement of the referenced polynucleotide sequence.

[53] The sixth column in Table 1A provides the corresponding SEQ ID NO:Y for the polypeptide sequence encoded by the preferred ORF delineated in column 5. In one embodiment, the invention provides an amino acid sequence comprising, or alternatively consisting of, a polypeptide encoded by the portion of SEQ ID NO:X delineated by "ORF (From-To)". Also provided are polynucleotides encoding such amino acid sequences and the complementary strand thereto.

[54] Column 7 in Table 1A lists residues comprising epitopes contained in the polypeptides encoded by the preferred ORF (SEQ ID NO:Y), as predicted using the algorithm of Jameson and Wolf, (1988) Comp. Appl. Biosci. 4:181-186. The Jameson-Wolf antigenic analysis was performed using the computer program PROTEAN (Version 3.11 for the Power MacIntosh, DNASTAR, Inc., 1228 South Park Street Madison, WI). In specific embodiments, polypeptides of the invention comprise, or alternatively consist of, at least one, two, three, four, five or more of the predicted epitopes as described in Table 1A. It will be appreciated that depending on the analytical criteria used to predict antigenic determinants, the exact address of the determinant may vary slightly.

[55] Column 8 in Table 1A provides an expression profile and library code: count for each of the contig sequences (SEQ ID NO:X) disclosed in Table 1A, which can routinely be combined with the information provided in Table 4 and used to determine the tissues, cells, and/or cell line libraries which predominantly express the polynucleotides of the invention. The first number in column 8 (preceding the colon), represents the tissue/cell source identifier code corresponding to the code and description provided in Table 4. For those identifier codes in which the first two letters are not "AR", the second number in column 8 (following the colon) represents the number of times a sequence corresponding to the reference polynucleotide sequence was identified in the tissue/cell source. Those tissue/cell source identifier codes in which the first two letters are "AR" designate information generated using DNA array technology. Utilizing this technology, cDNAs were amplified by PCR and then transferred, in duplicate, onto the array. Gene expression was assayed through hybridization of first strand cDNA probes to the DNA array. cDNA probes were generated from total RNA extracted from a variety of different tissues and cell lines. Probe synthesis was performed in the presence of ³³P dCTP, using oligo(dT) to prime reverse transcription. After hybridization, high stringency washing conditions were employed to remove non-specific hybrids from the array. The remaining signal, emanating from each gene target, was measured using a Phosphorimager. Gene expression was reported as Phosphor Stimulating Luminescence (PSL) which reflects the level of phosphor signal generated from the probe hybridized to each of the gene targets represented on the array. A local background signal subtraction was performed before the total signal generated from each array was used to normalize gene expression between the different hybridizations. The value presented after "[array code]:" represents the mean of the duplicate values, following background subtraction and probe normalization. One of skill in the art could routinely use this information to identify normal and/or diseased tissue(s) which show a predominant expression pattern of the corresponding polynucleotide of the invention or to identify polynucleotides which show predominant and/or specific tissue and/or cell expression.

[56] Column 9 in Table 1A provides a chromosomal map location for certain polynucleotides of the invention. Chromosomal location was determined by finding exact matches to EST and cDNA sequences contained in the NCBI (National Center for Biotechnology Information) UniGene database. Each sequence in the UniGene database is assigned to a "cluster"; all of the ESTs, cDNAs, and STSs in a cluster are believed to be derived from a single gene. Chromosomal mapping data is often available for one or more

sequence(s) in a UniGene cluster; this data (if consistent) is then applied to the cluster as a whole. Thus, it is possible to infer the chromosomal location of a new polynucleotide sequence by determining its identity with a mapped UniGene cluster.

[57] A modified version of the computer program BLASTN (Altshul et al., J. Mol. Biol. 215:403-410 (1990); and Gish and States, Nat. Genet. 3:266-272 (1993)) was used to search the UniGene database for EST or cDNA sequences that contain exact or near-exact matches to a polynucleotide sequence of the invention (the 'Query'). A sequence from the UniGene database (the 'Subject') was said to be an exact match if it contained a segment of 50 nucleotides in length such that 48 of those nucleotides were in the same order as found in the Query sequence. If all of the matches that met this criteria were in the same UniGene cluster, and mapping data was available for this cluster, it is indicated in Table 1A under the heading "Cytologic Band". Where a cluster had been further localized to a distinct cytologic band, that band is disclosed; where no banding information was available, but the gene had been localized to a single chromosome, the chromosome is disclosed.

[58] Once a presumptive chromosomal location was determined for a polynucleotide of the invention, an associated disease locus was identified by comparison with a database of diseases which have been experimentally associated with genetic loci. The database used was the Morbid Map, derived from OMIMTM (*supra*). If the putative chromosomal location of a polynucleotide of the invention (Query sequence) was associated with a disease in the Morbid Map database, an OMIM reference identification number was noted in column 10, Table 1A, labelled "OMIM Disease Reference(s)". Table 5 is a key to the OMIM reference identification numbers (column 1), and provides a description of the associated disease in Column 2.

TABLE 1B

| Clone ID
NO:Z | SEQ ID
NO:X | CONTIG
ID: | BAC ID: A | SEQ ID
NO:B | EXON
From-To |
|------------------|----------------|---------------|-----------|----------------|--|
| HFCBB56 | 24 | 910073 | AC068296 | 1268 | 1-225 |
| HIBBF63 | 75 | 912715 | AC009065 | 1269 | 1-70
850-1112
1169-1622
1707-1779
1874-1924
2836-2908
3006-4160 |
| HIBBF63 | 75 | 912715 | AC012171 | 1270 | 1-64
159-209
1122-1194
1292-1527
1593-2446 |
| HIBBF63 | 75 | 912715 | AC005346 | 1271 | 1-70
874-1136
1193-1646
1731-1803
1898-1948
2861-2933
3031-4185 |
| HIBBF63 | 75 | 912715 | AC009065 | 1272 | 1-547 |
| HIBBF63 | 75 | 912715 | AC012171 | 1273 | 1-547 |
| HIBBF63 | 75 | 912715 | AC009065 | 1274 | 1-424 |
| HIBBF63 | 75 | 912715 | AC005346 | 1275 | 1-547 |
| HIBBF63 | 75 | 912715 | AC012171 | 1276 | 1-419 |
| HIBBF63 | 75 | 912715 | AC005346 | 1277 | 1-424 |
| H2CBH45 | 90 | 963811 | AC068243 | 1278 | 1-267
1540-1640
3095-3380
3393-3556
3901-3967
4137-4639
5287-5856
5916-6588
7029-7876
8324-8414 |
| H2CBH45 | 90 | 963811 | AC068243 | 1279 | 1-309 |
| HBGQT03 | 93 | 908173 | AC024045 | 1280 | 1-218 |

| | | | | | |
|---------|-----|--------|----------|------|---|
| | | | | | 457-549
660-819
2039-2238
2529-2763
2876-3033
3631-3810
3941-4058
4184-4322
4727-4851
5161-6181 |
| HBGQT03 | 93 | 908173 | AC024045 | 1281 | 1-176 |
| HBGQT03 | 93 | 908173 | AC024045 | 1282 | 1-461
960-1030
1194-1959
2041-2516
3037-3122
3396-3455
4055-4366
4547-4599
4967-5216
5321-5461
6521-7174
7564-7841
8311-8758
8829-8969
8997-10118
10257-10910
12058-12385
12438-12953
13729-13873 |
| HCEPH71 | 97 | 522739 | AL365319 | 1283 | 1-494 |
| HCEPH71 | 97 | 522739 | AL390715 | 1284 | 1-494 |
| HCOOZ11 | 100 | 965306 | AL022238 | 1285 | 1-121
899-983
1445-1513
2166-3430
3550-3763
3859-3972
4449-4595
4960-5152
5385-5529 |

| | | | | | |
|---------|-----|--------|----------|------|--|
| | | | | | 5744-5972
6327-7067
7097-7152
7210-8073
8079-8680
8772-11399
12956-13517
13736-14155
14311-14753
16294-16357
16648-16806
16874-17059
17685-17787 |
| HCOOZ11 | 100 | 965306 | AL022238 | 1286 | 1-540 |
| HCOOZ11 | 100 | 965306 | AL022238 | 1287 | 1-665 |
| HCWFF88 | 101 | 506577 | AC025670 | 1288 | 1-300 |
| HCWFF88 | 101 | 506577 | AL157951 | 1289 | 1-624 |
| HCWFF88 | 101 | 506577 | AL157951 | 1290 | 1-409 |
| HCWFF88 | 101 | 506577 | AL157951 | 1291 | 1-83 |
| HDPFF24 | 104 | 909232 | AC020910 | 1292 | 1-353
359-468
787-861
1877-2199
4963-5089
5342-5440
6133-8734
9933-10319 |
| HDPFF24 | 104 | 909232 | AC020910 | 1293 | 1-814 |
| HDPFF24 | 104 | 909232 | AC020910 | 1294 | 1-437 |
| HDTKQ14 | 107 | 886936 | AL359542 | 1295 | 1-140
1249-4264 |
| HDTKQ14 | 107 | 886936 | AL023653 | 1296 | 1-140
1249-4264 |
| HDTKQ14 | 107 | 886936 | AL359542 | 1297 | 1-499 |
| HDTKQ14 | 107 | 886936 | AL359542 | 1298 | 1-145 |
| HDTKQ14 | 107 | 886936 | AL023653 | 1299 | 1-499 |
| HFTDF15 | 113 | 657020 | AL365277 | 1300 | 1-406 |
| HFTDF15 | 113 | 657020 | AC024511 | 1301 | 1-406 |
| HFTDF15 | 113 | 657020 | AL365277 | 1302 | 1-430 |
| HFTDF15 | 113 | 657020 | AC024511 | 1303 | 1-430 |
| HFTDF15 | 113 | 657020 | AL365277 | 1304 | 1-526 |

| | | | | | |
|---------|-----|--------|----------|------|--|
| HFTDF15 | 113 | 657020 | AC024511 | 1305 | 1-526 |
| HLQDT35 | 117 | 839777 | AC010998 | 1306 | 1-44
540-884
1203-1261
1994-2178
2303-2474
2991-3088
3592-3757
4262-4364
4742-5802
6235-7057
7126-8472 |
| HLQDT35 | 117 | 839777 | AC013357 | 1307 | 1-44
540-884
1203-1261
1994-2178
2303-2474
2991-3088
3592-3757
4262-4364
4742-5802
6235-7057
7126-8472 |
| HLQDT35 | 117 | 839777 | AC010998 | 1308 | 1-768 |
| HLQDT35 | 117 | 839777 | AC013357 | 1309 | 1-6035
8430-11057 |
| HLQDT35 | 117 | 839777 | AC010998 | 1310 | 1-278 |
| HLQDT35 | 117 | 839777 | AC013357 | 1311 | 1-278 |
| HLWFN63 | 118 | 908437 | AC006599 | 1312 | 1-30
1525-1711
5428-5502
7038-7273
7590-7735
8960-9049
11665-11800
12889-13194
13907-14119
14889-15043
15926-16164
18759-19079
20581-20693 |

| | | | | | |
|---------|-----|--------|----------|------|--|
| | | | | | 22531-22783
23817-24956
26153-26283
26791-27141
28145-29220 |
| HLWFN63 | 118 | 908437 | AL033378 | 1313 | 1-30
1525-1711
5428-5502
7038-7261
7590-7735
11665-11800
12889-13194
13907-14119
14889-15043
15926-16164
18759-19079
20581-20693
22531-22753
23817-24956
26153-26283
26791-27141
28145-29220 |
| HLWFN63 | 118 | 908437 | AC006599 | 1314 | 1-2939 |
| HLWFN63 | 118 | 908437 | AL033378 | 1315 | 1-2939 |
| HMSCD15 | 120 | 918133 | AC027008 | 1316 | 1-1190 |
| HMSCD15 | 120 | 918133 | AL158207 | 1317 | 1-130
923-1252
1765-3269
4138-4483
6546-7734 |
| HMSCD15 | 120 | 918133 | AL158207 | 1318 | 1-371 |
| HPMFL08 | 128 | 959569 | Z93016 | 1319 | 1-477 |
| HPMFL08 | 128 | 959569 | Z93016 | 1320 | 1-650 |
| HTEAG49 | 135 | 954614 | AL390796 | 1321 | 1-1310 |
| HTEAG49 | 135 | 954614 | AL357045 | 1322 | 1-1310 |
| HTEAG49 | 135 | 954614 | AL390796 | 1323 | 1-627 |
| HTEAG49 | 135 | 954614 | AL357045 | 1324 | 1-627 |
| HTLBH67 | 136 | 751985 | AC008439 | 1325 | 1-62
293-400
452-976
1016-1058 |

| | | | | | |
|---------|-----|--------|----------|------|---|
| | | | | | 1463-1534
1886-2026
2110-2249
2401-2463
3324-4027
4192-4288
4694-5330
5485-5650
5813-6262
6273-6401
6475-6559
6728-6847
6979-7205
7573-7676
7730-8146
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| HHEHC53 | 209 | 921783 | AC009427 | 1369 | 1-100
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| HMCV88 | 347 | 924874 | AC005476 | 1439 | 1-366 |
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| HFVHV40 | 349 | 945849 | AC020911 | 1442 | 1-110 |
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| HTSFJ40 | 364 | 722406 | AC006171 | 1454 | 1-247
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| HSDJH12 | 368 | 876344 | AL359882 | 1458 | 1-283
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| HSDJH12 | 368 | 876344 | AC046143 | 1459 | 1-283
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20861-21075
22489-22727
22961-23073
25307-25360
29573-29961
31051-31168 |
| HOUBZ94 | 376 | 527876 | AC005954 | 1465 | 1-131 |
| HCE3W04 | 379 | 615501 | AC022366 | 1466 | 1-565
1503-1718
1838-1933
2011-2097
2265-2335
2588-2693
2905-2975
3090-3726
3809-3889
4080-4591
4847-5070
5355-5819 |

| | | | | | |
|---------|-----|--------|----------|------|--|
| HCE3W04 | 379 | 615501 | AC022506 | 1467 | 1-563
1501-1716
1836-1931
2009-2094
2263-2333
2586-2691
2903-2973
3088-3724
3807-3887
4085-4540 |
| HCE3W04 | 379 | 615501 | AC025165 | 1468 | 1-565
1503-1718
1838-1933
2011-2097
2265-2335
2588-2693
2905-2975
3090-3726
3809-3889
4080-4591
4847-5070
5355-5819 |
| HCE3W04 | 379 | 615501 | AC025165 | 1469 | 1-604 |
| HCE3W04 | 379 | 615501 | AC022506 | 1470 | 1-518
999-1533
1563-1830
2015-2094
2441-3538
4095-4315
4655-5378 |
| HPJAP28 | 382 | 686349 | AC004794 | 1471 | 1-599
769-987
1562-1690
1879-2043
2595-2821
3807-5923
6102-6572
6644-7502
8127-8585
9415-9553
9669-9763 |

| | | | | | |
|----------|-----|--------|----------|------|---|
| | | | | | 9826-9989
10230-10322 |
| HPJAP28 | 382 | 686349 | AC004794 | 1472 | 1-97
1121-1975 |
| HPJAP28 | 382 | 686349 | AC004794 | 1473 | 1-691 |
| HIBEC79 | 383 | 703000 | AC011458 | 1474 | 1-138
397-1114
1356-1693
1781-2091
2270-2389
2474-2908
3053-3202
3288-3349
3421-3976
4551-4662
4696-5053
5166-5246
5318-5490
5592-5723
6082-6283
6619-6733
6853-6942
7491-7586
7922-8003
8015-8421
8432-8624
8714-8856
8943-10332
10482-10901
11647-11934
13110-13177
13310-14175 |
| HIBEC79 | 383 | 703000 | AC011458 | 1475 | 1-406 |
| HIBEC79 | 383 | 703000 | AC011458 | 1476 | 1-287 |
| HNFS82 | 387 | 779946 | AC010835 | 1477 | 1-418 |
| HFPBB28 | 389 | 844526 | AC016135 | 1478 | 1-845 |
| HFPBB28 | 389 | 844526 | AC018512 | 1479 | 1-776 |
| HFPBB28 | 389 | 844526 | AC073717 | 1480 | 1-240 |
| HFPBB28 | 389 | 844526 | AC002518 | 1481 | 1-150 |
| HDQGGZ78 | 399 | 909735 | AC026282 | 1482 | 1-238
976-1440 |

| | | | | | |
|---------|-----|--------|----------|------|--|
| | | | | | 2143-2356
6769-6910
9591-9648
9951-10098 |
| HSIDQ38 | 401 | 909854 | AC003070 | 1483 | 1-152
3039-3473
4301-4483
4678-4795
5280-5944
6055-6117
6290-6359
6677-6761
8475-9284
11404-11918
12112-12437
12443-13065
13153-13467
13593-13719
13799-14185
14224-16489 |
| HFTBL33 | 407 | 910055 | AC022366 | 1484 | 1-565
1503-1718
1838-1933
2011-2097
2265-2335
2588-2693
2905-2975
3090-3726
3809-3889
4080-4591
4847-5070
5355-5819 |
| HFTBL33 | 407 | 910055 | AC025165 | 1485 | 1-565
1503-1718
1838-1933
2011-2097
2265-2335
2588-2693
2905-2975
3090-3726
3809-3889 |

| | | | | | |
|---------|-----|--------|----------|------|--|
| | | | | | 527-599
798-868
958-1095
1196-1260
1465-1577
1652-1732
2256-3158
4031-4899
4984-5306
5735-6066
6554-6694
6780-6970
7107-7232
7316-7404
7529-7643
7744-7917
8401-8592
8675-8813
9685-9920
9958-10211
10485-11014
11088-11199
11958-15576
16324-16465
16587-16818
16939-17000
17440-17554
17558-17946
18645-18765
19015-19378
20522-20937
22111-22452 |
| HWAF84 | 412 | 911559 | AC004151 | 1490 | 1-134 |
| HWADR60 | 416 | 926487 | AC023176 | 1491 | 1-178
293-506
542-940
1591-2005
2031-2104
2390-2509
3681-3797
4018-4165 |

| | | | | | |
|---------|-----|--------|----------|------|---|
| | | | | | 4267-4381
4704-4736 |
| HWADR60 | 416 | 926487 | AC023176 | 1492 | 1-162
443-739
1067-1458
1745-1877
1976-2119
2816-2883
3171-3294
3727-4154
4340-4442
5251-6126
6708-7176
7418-7880
8134-8752
9979-10164
11234-11413
12532-12666
13313-13459
14761-14898
15208-15308
16207-16518 |
| HPCIG66 | 419 | 930886 | AC024888 | 1493 | 1-36
149-234
537-623
852-921
1077-1728 |
| HPCIG66 | 419 | 930886 | AC024888 | 1494 | 1-61
133-210
992-1107
1310-1644
1834-1905
2133-2254
2927-3032
4154-4254
4482-4683 |
| HPCIG66 | 419 | 930886 | AC024888 | 1495 | 1-63
239-327
574-1064
1763-2190
2394-2604 |

| | | | | | |
|---------|-----|--------|----------|------|---|
| | | | | | 2659-2795
3452-4040
5967-6046
6187-6254 |
| HCRPU72 | 420 | 931140 | AC023151 | 1496 | 1-65
721-1042 |
| HE9RT95 | 421 | 934556 | AC008439 | 1497 | 1-57
311-418
1581-1904
2176-2322
2625-2690
3445-3950
5254-5425
5466-5980
6002-6037
6169-6228
6339-6480
6701-6739
7238-7349
7664-8821 |
| HE9RT95 | 421 | 934556 | AC022420 | 1498 | 1-323
1372-1431
1657-1821
2377-2485
4488-4700
4954-5061
6224-6547
6819-6965
7268-7333
8088-8593
9897-10068
10109-10623
10645-10680
10812-10871
10982-11123
11345-11383
11877-12000
12310-13467 |
| HE9RT95 | 421 | 934556 | AC022420 | 1499 | 1-389 |
| HE9RT95 | 421 | 934556 | AC022420 | 1500 | 1-62
295-403 |

| | | | | | |
|---------|-----|--------|----------|------|--|
| | | | | | 455-979
1019-1061
1466-1537
1890-2030
2114-2253
2405-2467
3328-4030
4195-4291
4697-5333
5488-5653
5816-6265
6276-6404
6478-6562
6731-6850
6982-7208
7575-7678
7732-8148
8195-8864
8885-9392
9590-9721
9859-10754
10980-11014
11126-12121 |
| HWADD57 | 426 | 943039 | AC011492 | 1501 | 1-303
949-1648
1913-2937
3032-3231
3325-3443
4093-4485
4777-4936
5057-5548
5650-5968 |
| HWADD57 | 426 | 943039 | AC011492 | 1502 | 1-50
852-907
988-1407
1584-1839
2455-2586
2689-2787 |
| HFKHR40 | 431 | 952470 | AC018805 | 1503 | 1-525
612-1372
1476-1730 |

| | | | | | |
|---------|-----|--------|----------|------|--|
| | | | | | 1732-2155
2345-2460
2652-3025
3157-3251
3449-3540
3680-3780
3914-4131
4215-4491
4603-4741
4913-4987
5135-5190
5435-5571
5901-6011
6309-6423
6922-8294
8370-8522 |
| HFKHR40 | 431 | 952470 | AC061707 | 1504 | 1-527
614-1374
1478-1732
1734-2158
2348-2463
2655-3027
3159-3253
3451-3542
3682-3782
3916-4134
4219-4495
4607-4745
4917-4991
5139-5194
5439-5575
5905-6015
6313-6427
6926-9300
9919-9960
10029-10186
11393-11624
12094-12294
13227-13375
13690-13829
13921-14010 |

| | | | | | |
|---------|-----|--------|----------|------|--|
| | | | | | 14362-14486 |
| HFKHR40 | 431 | 952470 | AC018805 | 1505 | 1-343
700-770 |
| HFKHR40 | 431 | 952470 | AC061707 | 1506 | 1-343
700-771 |
| HFKHR40 | 431 | 952470 | AC061707 | 1507 | 1-277 |
| HWLHF10 | 435 | 963422 | AC010545 | 1508 | 1-40
1661-1891
2119-2199
5160-5349
6239-6607
7675-8566
9450-9516
9675-9752
10110-10274
14154-15055
16384-16500
17055-17139
19941-20453
20703-21216
21806-21945
23638-24171
24527-24795
25564-25656
26644-26787
27284-27438
28354-28612
29247-29591
29597-30208
32018-32539
33187-33942 |
| HWLHF10 | 435 | 963422 | AC010545 | 1509 | 1-721 |
| HWLHF10 | 435 | 963422 | AC010545 | 1510 | 1-610
675-1454
1591-2267
2801-3363 |

[59] Table 1B summarizes additional polynucleotides encompassed by the invention (including cDNA clones related to the sequences (Clone ID NO:Z), contig sequences (contig identifier (Contig ID:) contig nucleotide sequence identifiers (SEQ ID NO:X)), and genomic sequences (SEQ ID NO:B). The first column provides a unique clone identifier, "Clone ID NO:Z", for a cDNA clone related to each contig sequence. The second column provides the sequence identifier, "SEQ ID NO:X", for each contig sequence. The third column provides a unique contig identifier, "Contig ID:" for each contig sequence. The fourth column, provides a BAC identifier "BAC ID NO:A" for the BAC clone referenced in the corresponding row of the table. The fifth column provides the nucleotide sequence identifier, "SEQ ID NO:B" for a fragment of the BAC clone identified in column four of the corresponding row of the table. The sixth column, "Exon From-To", provides the location (i.e., nucleotide position numbers) within the polynucleotide sequence of SEQ ID NO:B which delineate certain polynucleotides of the invention that are also exemplary members of polynucleotide sequences that encode polypeptides of the invention (e.g., polypeptides containing amino acid sequences encoded by the polynucleotide sequences delineated in column six, and fragments and variants thereof).

TABLE 2

| Clone ID
NO:Z | Contig
ID: | SEQ
ID
NO:X | Analysis
Method | PFam/NR Description | PFam/NR Accession
Number | Score/
Percent
Identity | NT From | NT To |
|------------------|---------------|-------------------|----------------------------|---|-------------------------------|--|---|--|
| HDPTE21 | 1165861 | 11 | blastx.14 | (AB018414) Gab2 [Mus
musculus] | gi 4589377 dbj BAA7
6738.1 | 74%
50%
55%
65%
68%
69%
66%
39%
32%
45%
36%
34% | 51
246
1650
1344
1620
1188
1260
1527
1017
1182
1528
2907 | 227
416
1784
1421
1667
1226
1295
1595
1100
1241
1584
2984 |
| HDPTE21 | 887711 | 443 | HMMER
2.1.1 | PFAM: PH domain | PF00169 | 25.2 | 31 | 129 |
| H6EDR51 | 930788 | 445 | HMMER
2.1.1
blastx.2 | PFAM: PH domain
(AF053974) SWAP-70
[Mus musculus] | PF00169
gb AAC40155.1 | 80.9
53%
57%
26%
19%
43%
33% | 664
19
1291
1464
1566
1199
1214 | 951
996
1395
1760
1826
1279
1285 |
| HAPRA41 | 1154054 | 13 | blastx.14 | actin filament-associated
protein [Gallus gallus] | gi 487418 gb AAA18
166.1 | 82% | 53 | 1261 |
| HAPRA41 | 926285 | 446 | HMMER
2.1.1 | PFAM: PH domain | PF00169 | 59.8 | 111 | 398 |

| | | | blastx.2 | actin filament-associated protein [Gallus gallus] | gb AAA18166.1 | 76% | 45 | 473 |
|---------|---------|-----|-------------|---|-------------------------------------|-------------|-------------|---------------|
| HBXBI07 | 954118 | 447 | HMMER 2.1.1 | PFAM: PH domain | PF00169 | 33.2 | 164 | 484 |
| | | | blastx.2 | (AF101054) PHR1 isoform 2 [Homo sapiens] | gb AAF18572.1 AF101054_1 | 100% 92% | 119 684 | 637 722 |
| HBXCM38 | 910086 | 15 | HMMER 1.8 | PFAM: Src homology domain 3 | PF00018 | 55.89 | 1062 | 1232 |
| | | | blastx.2 | unnamed protein product [unidentified] | emb CAB69447.1 | 92% 87% 77% | 402 13 1295 | 1316 396 1348 |
| HCE3E50 | 961098 | 448 | HMMER 1.8 | PFAM: PH (pleckstrin homology) domain | PF00169 | 50.5 | 146 | 448 |
| HCEQD04 | 1150868 | 17 | blastx.14 | (AF163255) adaptor protein DAPP1 [Mus musculus] | gi 5733602 gb AAD49698.1 AF163255_1 | 36% | 30 | 278 |
| HCEQD04 | 927873 | 449 | HMMER 2.1.1 | PFAM: PH domain | PF00169 | 44.9 | 139 | 258 |
| | | | blastx.2 | (AF163255) adaptor protein DAPP1 [Mus musculus] | gb AAD49698.1 AF163255_1 | 37% | 7 | 270 |
| HDPHI92 | 909900 | 18 | HMMER 2.1.1 | PFAM: RhoGAP domain | PF00620 | 235.1 | 888 | 1343 |
| | | | blastx.2 | racGAP [Dictyostelium discoideum] | emb CAA71241.1 | 37% | 825 | 1343 |
| HDPLT89 | 962403 | 19 | HMMER 2.1.1 | PFAM: Src homology domain 2 | PF00017 | 85.1 | 194 | 418 |
| | | | blastx.2 | (AF163254) adaptor protein DAPP1 [Homo sapiens] | gb AAD49697.1 AF163254_1 | 100% | 92 | 931 |
| HDPSU48 | 1228284 | 20 | blastx.14 | hypothetical protein | pir T13601 T13601 | 56% | 421 | 873 |

| | | | | | | | | |
|---------|---------|-----|----------------------------|---|-------------------|-------|------|------|
| HDPSU48 | 909949 | 450 | HMMER
2.1.1
blastx.2 | 80H7.5 - fruit fly
(Drosophila melanogaster)
PFAM: FYVE zinc finger | PF01363 | 72% | 243 | 485 |
| | | | | (AL031027)
/prediction=(method:""ge
nefinder"" , 1 1 1
PROTEIN)"" , sp | emb CAA19842.1 | 70% | 230 | 862 |
| HDPWE80 | 909916 | 21 | HMMER
2.1.1
blastx.2 | PFAM: PH domain | PF00169 | 81.2 | 412 | 708 |
| | | | | (AF102854) membrane-
associated guanylate
kinase-interacting protein
2 Maguin-2 [Rattus
norvegicus] | gb AAD04568.1 | 36% | 349 | 756 |
| HDQFY84 | 971615 | 451 | HMMER
2.1.1 | PFAM: PH domain | PF00169 | 52.1 | 1232 | 1507 |
| HEONQ19 | 930705 | 23 | HMMER
2.1.1
blastx.2 | PFAM: PH domain | PF00169 | 42.5 | 213 | 533 |
| | | | | (AJ250425) Collybistin I
[Rattus norvegicus] | emb CAB65966.1 | 96% | 9 | 629 |
| HFCBB56 | 910073 | 24 | HMMER
1.8
blastx.2 | PFAM: EF hand | PF00036 | 23.95 | 431 | 514 |
| | | | | 1-phosphatidylinositol-
4,5-bisphosphate
phosphodiesterase 1 | pir S14113 S14113 | 36% | 275 | 565 |
| HFKKZ94 | 926486 | 452 | HMMER
2.1.1 | PFAM: PH domain | PF00169 | 55.3 | 226 | 558 |
| HHBGJ53 | 909912 | 453 | HMMER
2.1.1 | PFAM: PH domain | PF00169 | 38.3 | 160 | 267 |
| HHFJF24 | 1212624 | 27 | blastx.14 | GUANINE | sp Q64096 DBS MO | 83% | 3 | 566 |

| | | | | NUCLEOTIDE
EXCHANGE FACTOR
DBS (DBLS BIG
SISTER) (MCF2
TRANSFORMING
SEQUENCE-LIKE
PROTEIN). | USE | 71%
79%
23% | 545
878
512 | 811
979
613 |
|---------|---------|-----|----------------------------|--|----------------------------------|-------------------|-------------------|-------------------|
| HHFJF24 | 910065 | 454 | HMMER
1.8
blastx.2 | PFAM: PH (pleckstrin
homology) domain
GUANINE
NUCLEOTIDE
EXCHANGE FACTOR
DBS (DBL'S BIG
SISTER) 1
(FRAGMENT). | PF00169
sp Q63406 DBS_RA
T | 23.24
98% | 3
3 | 107
158 |
| HHFMM10 | 1178801 | 28 | blastx.14 | putative [Rattus
norvegicus] | gi 397579 emb CAA5
2297.1 | 97%
91% | 138
503 | 263
613 |
| HHFMM10 | 962997 | 455 | HMMER
2.1.1
blastx.2 | PFAM: PH domain
putative [Rattus
norvegicus] | PF00169
emb CAA52297.1 | 42.9
95% | 251
131 | 487
493 |
| HHPBA42 | 901921 | 29 | HMMER
2.1.1
blastx.2 | PFAM: PH domain
mitogen inducible gene
mig-2 [Homo sapiens] | PF00169
emb CAA80852.1 | 42.4
61% | 352
1 | 663
822 |
| HHPSP89 | 910024 | 456 | HMMER
2.1.1
blastx.2 | PFAM: PH domain
(AB023656) KIF1B-beta
[Mus musculus] | PF00169
dbj BAA75243.1 | 62.3
87% | 562
118 | 855
906 |
| HKABX13 | 1167182 | 31 | blastx.14 | (AK000790) unnamed
protein product [Homo
sapiens] | gi 7021093 dbj BAA9
1379.1 | 98%
57% | 97
589 | 480
786 |

| | | | | | | | | |
|----------|---------|-----|-----------------------------|---|------------------------------|------------|------------|------------|
| HKABX13 | 958656 | 457 | HMMER
1.8
blastx.2 | PFAM: PH (pleckstrin
homology) domain
(AK000790) unnamed
protein product [Homo
sapiens] | PF00169 | 51.8 | 104 | 424 |
| HLTHG77 | 878592 | 458 | HMMER
2.1.1
blastx.2 | PFAM: PH domain
(AK001472) unnamed
protein product [Homo
sapiens] | PF00169 | 60.2 | 1254 | 1625 |
| HLWBZ09 | 957912 | 459 | HMMER
1.8
blastx.14 | PFAM: PH (pleckstrin
homology) domain | PF00169 | 21.29 | 145 | 417 |
| HLWEH54 | 932133 | 460 | HMMER
2.1.1
blastx.14 | PFAM: PH domain | PF00169 | 114.1 | 556 | 849 |
| HL YAA41 | 1188029 | 35 | HMMER
2.1.1
blastx.14 | SecG [Dictyostelium
discoideum] | gi 1688318 gb AAB3
6958.1 | 43% | 173 | 352 |
| HL YAA41 | 909874 | 461 | HMMER
2.1.1
blastx.14 | PFAM: PH domain | PF00169 | 37.3 | 162 | 260 |
| HL YDV62 | 1154065 | 36 | HMMER
2.1.1
blastx.14 | SecG [Dictyostelium
discoideum] | gi 1688318 gb AAB3
6958.1 | 43% | 173 | 352 |
| HL YDV62 | 927872 | 462 | HMMER
2.1.1
blastx.2 | PFAM: PH domain
(AC005496) unknown
protein [Arabidopsis
thaliana] | PF00169 | 58.6 | 188 | 406 |
| HMCFB47 | 910088 | 463 | HMMER
2.1.1
blastx.2 | PFAM: PH domain
(AB005903) AtPH1
[Arabidopsis thaliana] | PF00169 | 41%
38% | 113
451 | 292
504 |
| HMSOI20 | 928168 | 464 | HMMER
1.8 | PFAM: PH (pleckstrin
homology) domain | PF00169 | 73 | 79 | 378 |
| | | | | | dbj BAA84651.1 | 30% | 85 | 375 |
| | | | | | | 18.44 | 154 | 384 |

| | | | | | | | | |
|---------|---------|-----|----------------------------|---|---|----------------------------------|-------------------------------|--------------------------------|
| HOENH55 | 1163460 | 39 | blastx.14 | p116Rip [Mus musculus] | gi 1657837 gb AAB18198.1 | 95%
86%
100%
80%
40% | 343
1
139
220
293 | 624
90
207
294
358 |
| HOENH55 | 922141 | 465 | HMMER
2.1.1 | PFAM: PH domain | PF00169 | 50.5 | 406 | 621 |
| HP1A101 | 1078178 | 40 | blastx.2
blastx.14 | p116Rip [Mus musculus]
unnamed protein product
[unidentified] | gb AAB18198.1
gi 4756912 emb CAB42323.1 | 76%
36%
42%
72% | 1
213
414
183 | 624
437
476
215 |
| HP1A101 | 909928 | 466 | HMMER
2.1.1 | PFAM: PH domain | PF00169 | 30.3 | 294 | 482 |
| HPJCT50 | 919836 | 467 | blastx.2
HMMER
2.1.1 | unnamed protein product
[unidentified]
PFAM: PH domain | emb CAB42187.1
PF00169 | 62%
81.4 | 10
728 | 195
1015 |
| HPMFE91 | 1164740 | 42 | blastx.14 | (AF210818) SWAP-70
[Homo sapiens]
(AF136450) goodpasture
antigen-binding protein
[Homo sapiens] | gb AAF24486.1 AF210818_1
gi 4835895 gb AAD30288.1 AF136450_1 | 85%
89%
97% | 98
20
1097 | 1453
1129
1813 |
| HPMFE91 | 910026 | 468 | HMMER
2.1.1 | PFAM: PH domain | PF00169 | 81.9 | 332 | 613 |
| HRAED51 | 1090522 | 43 | blastx.2 | (AF136450) goodpasture
antigen-binding protein
[Homo sapiens]
racGAP [Dictyostelium
discoideum] | gb AAD30288.1 AF136450_1
gi 2190355 emb CAA71241.1 | 94%
40%
48% | 263
363
195 | 955
569
305 |
| HRAED51 | 909859 | 469 | HMMER
2.1.1 | PFAM: RhoGAP domain | PF00620 | 78.3 | 259 | 504 |

| | | | | | | | | |
|---------|---------|-----|-------------|--|---------------------------|---------------------------------|---------------------------------|-----------------------------------|
| HSMBA19 | 924885 | 470 | blastx.2 | beta-chimaerin [Rattus norvegicus] | gb AAA40809.1 | 28% | 259 | 585 |
| | | | HMMER 2.1.1 | PFAM: PH domain | PF00169 | 34.3 | 289 | 528 |
| | | | blastx.2 | (AL096767) dJ579N16.2 (SET binding factor 1) [Homo sapiens] | emb CAB63063.1 | 49%
76% | 4
533 | 531
607 |
| HSYCY88 | 914775 | 45 | HMMER 2.1.1 | PFAM: PH domain | PF00169 | 34.6 | 811 | 966 |
| | | | blastx.2 | putative [Rattus norvegicus] | emb CAA52297.1 | 97%
63%
88%
50%
44% | 607
21
425
962
1041 | 966
437
532
1111
1136 |
| | | | HMMER 2.1.1 | PFAM: FYVE zinc finger | PF01363 | 88.9 | 321 | 521 |
| HTEKD92 | 1090524 | 47 | blastx.2 | (AF038388) actin-filament binding protein Frabin [Rattus norvegicus] | gb AAC27698.1 | 89%
51% | 57
1 | 959
81 |
| | | | blastx.14 | (AK000074) unnamed protein product [Homo sapiens] | gi 7019925 dbj BAA90927.1 | 87% | 482 | 1165 |
| | | | HMMER 2.1.1 | PFAM: PH domain | PF00169 | 54.1 | 252 | 530 |
| HTLDT05 | 909752 | 472 | blastx.2 | (AK000074) unnamed protein product [Homo sapiens] | dbj BAA90927.1 | 87% | 468 | 1151 |
| | | | HMMER 2.1.1 | PFAM: PH domain | PF00169 | 36.9 | 59 | 271 |
| | | | blastx.2 | (AK000004) FLJ00004 protein [Homo sapiens] | dbj BAA92229.1 | 77% | 47 | 487 |

| | | | | | | | | |
|---------|---------|-----|----------------------------|---|-------------------------------|--|---|---|
| HTPDS90 | 529764 | 473 | HMMER
2.1.1
blastx.2 | PFAM: PH domain
putative [Rattus
norvegicus] | PF00169
emb CAA52297.1 | 65.3 | 132 | 440 |
| HTPHM71 | 1194698 | 50 | blastx.14 | CDNA FLJ20260 FIS,
CLONE COLF7627. | sp BAA91043 BAA9
1043 | 62%
70%
42%
59%
47%
23%
42%
80%
27%
38% | 61
1423
520
1192
700
889
1054
808
1552
600 | 348
1659
675
1287
762
1002
1131
837
1671
653 |
| HTPHM71 | 909878 | 474 | HMMER
1.8
blastx.2 | PFAM: PH (pleckstrin
homology) domain
(AK000267) unnamed
protein product [Homo
sapiens] | PF00169
dbj BAA91043.1 | 38.8 | 57 | 341 |
| HUAR12 | 944393 | 475 | HMMER
2.1.1
blastx.2 | PFAM: PH domain
(AB008430) CDEP
[Homo sapiens] | PF00169
dbj BAA24267.1 | 63.5 | 69 | 359 |
| HWAGP22 | 1150195 | 52 | blastx.14 | (AL031027)
/prediction=(method:""ge
nefinder""; 1 1 1
PROTEIN)""; sp | gi 3292902 emb CAA
19842.1 | 45% | 3 | 677 |
| HWAGP22 | 909919 | 476 | HMMER
2.1.1
blastx.2 | PFAM: FYVE zinc finger
(AL031027) | PF01363
emb CAA19842.1 | 50% | 1653 | 1021 |
| HWAGP22 | 909919 | 476 | HMMER
2.1.1
blastx.2 | PFAM: FYVE zinc finger
(AL031027) | PF01363
emb CAA19842.1 | 89.9 | 516 | 716 |
| HWAGP22 | 909919 | 476 | HMMER
2.1.1
blastx.2 | PFAM: FYVE zinc finger
(AL031027) | PF01363
emb CAA19842.1 | 50% | 78 | 710 |

| | | | | /prediction=(method:""ge
finder""", 1 1 1
PROTEIN)""", sp | | | | | |
|---------|---------|-----|----------------------------|--|---|---|--|---|--|
| HWBCE37 | 906968 | 53 | HMMER
1.8
blastx.2 | PFAM: PH (pleckstrin
homology) domain
brain beta spectrin [Mus
musculus] | PF00169 | 60.73 | 39 | 353 | |
| HWLFB60 | 1223499 | 54 | blastx.14 | CG1513 PROTEIN. | gb AAC42040.1
sp Q9V5D4 Q9V5D4 | 30% | 93 | 386 | |
| | | | | | | 64%
72%
66%
33%
52%
24%
38% | 1445
1127
2
1943
518
1295
89 | 1924
1459
355
2218
580
1393
142 | |
| HWLFB60 | 910018 | 477 | HMMER
2.1.1
blastx.2 | PFAM: PH domain
(AF000195) Contains
similarity to Pfam
domain: PF00169 (PH), 1 | PF00169 | 43 | 8 | 241 | |
| | | | | | gb AAC24270.1 | 63%
33% | 14
238 | 241
414 | |
| HDPGS16 | 909833 | 478 | HMMER
1.8
blastx.2 | PFAM: Protein kinase C
terminal domain
(AJ245709) Akt-3 protein
[Homo sapiens] | PF00433 | 57.51 | 287 | 445 | |
| HDQDV69 | 937850 | 56 | HMMER
2.1.1
blastx.2 | PFAM: Eukaryotic protein
kinase domain
(AF169035) protein
kinase [Homo sapiens] | emb CAB53537.1
PF00069 | 100%
100%
212.5 | 236
3
68 | 460
116
598 | |
| HE6BK63 | 1153879 | 57 | blastx.14 | (AF128625) CDC42-
binding protein kinase
beta [Homo sapiens] | gb AAF12758.1 AF1
69035_1
gi 5006445 gb AAD3
7506.1 AF128625_1 | 98%
99% | 68
6 | 829
767 | |
| HE6BK63 | 661045 | 480 | HMMER | PFAM: Protein kinase C | PF00433 | 21.1 | 679 | 765 | |

| | | | 2.1.1 | terminal domain | | | | |
|---------|---------|-----|-----------|---|-------------------------------------|--------|------|------|
| | | | blastx.2 | (AF128625) CDC42-binding protein kinase beta [Homo sapiens] | gb AAD37506.1 AF128625_1 | 97% | 589 | 1179 |
| | | | | | | 99% | 101 | 595 |
| | | | | | | 23% | 862 | 1152 |
| | | | | | | 18% | 922 | 1140 |
| | | | | | | 25% | 937 | 1152 |
| | | | | | | 22% | 934 | 1170 |
| | | | | | | 22% | 904 | 1161 |
| HE6BK63 | 974253 | 481 | blastx.14 | (AF128625) CDC42-binding protein kinase beta [Homo sapiens] | gi 5006445 gb AAD37506.1 AF128625_1 | 99% | 2 | 328 |
| | | | | | | 66% | 357 | 500 |
| | | | | | | 100% | 502 | 570 |
| | | | | | | 22% | 137 | 325 |
| | | | | | | 100% | 330 | 362 |
| | | | | | | 55% | 325 | 378 |
| | | | | | | 32% | 242 | 325 |
| | | | | | | 53% | 523 | 561 |
| HFKDR14 | 974255 | 58 | HMMER 1.8 | PFAM: Eukaryotic protein kinase domain | PF00069 | 244.21 | 297 | 1097 |
| | | | blastx.2 | (AF128625) CDC42-binding protein kinase beta [Homo sapiens] | gb AAD37506.1 AF128625_1 | 98% | 72 | 1733 |
| | | | | | | 22% | 1572 | 1706 |
| HFPER82 | 1152249 | 59 | blastx.14 | (AC004877) sco-spondin-mucin-like; similar to P98167 l sapiens] | gi 3638957 gb AAC36301.1 | 68% | 137 | 90 |
| | | | | | | 34% | 227 | 123 |
| | | | | | | 42% | 569 | 513 |
| | | | | | | 50% | 387 | 346 |
| | | | | | | 34% | 332 | 255 |
| | | | | | | 54% | 84 | 52 |
| HFPER82 | 909835 | 482 | HMMER 1.8 | PFAM: Protein kinase C terminal domain | PF00433 | 33.87 | 943 | 1047 |
| | | | blastx.2 | human protein kinase B [Homo sapiens] | emb CAA43372.1 | 89% | 943 | 1053 |
| HAAAO58 | 1091088 | 60 | blastx.14 | (AF097887) Chp [Rattus | gi 3806122 gb AAC6 | 100% | 75 | 260 |

| | | | | | | | | |
|---------|---------|-----|----------------------------|---|--|--------------------------|------------------------|-------------------------|
| HAAA058 | 912622 | 483 | HMMER
2.1.1
blastx.2 | norvegicus]
PFAM: Ras family | 9198.1]
PF00071 | 85.9 | 75 | 365 |
| HADFK69 | 1091937 | 61 | blastx.14 | (AF097887) Chp [Rattus
norvegicus] | gb AAC69198.1 | 98% | 75 | 467 |
| HADFK69 | 912850 | 484 | HMMER
1.8
blastx.2 | (AF229839) kappa B-ras
1 [Homo sapiens]
PFAM: Ras family
(contains ATP/GTP
binding P-loop) | gi 7008402 gb AAF34
998.1
PF00071 | 91%
85.8 | 207
109 | 752
573 |
| HDPMO62 | 1152329 | 62 | blastx.14 | (AF229839) kappa B-ras
1 [Homo sapiens]
rab-related GTP-binding
protein [Homo sapiens] | gb AAF34998.1
gi 1491714 emb CAA
68227.1 | 90%
38%
64%
50% | 49
303
145
31 | 543
596
303
96 |
| HDPMO62 | 912722 | 485 | HMMER
1.8
blastx.2 | PFAM: Ras family
(contains ATP/GTP
binding P-loop) | PF00071 | 132.39 | 127 | 432 |
| HDPMO85 | 912837 | 486 | HMMER
1.8
blastx.2 | rab-related GTP-binding
protein [Homo sapiens]
PFAM: Ras family
(contains ATP/GTP
binding P-loop) | emb CAA68227.1
PF00071 | 54%
57%
75.28 | 133
20
162 | 444
76
668 |
| HDPUY72 | 966153 | 487 | HMMER
2.1.1
blastx.2 | (AF229840) kappa B-ras
2 [Homo sapiens]
PFAM: Ras family | gb AAF34999.1
PF00071 | 92%
325.7 | 147
815 | 719
207 |
| HDTJF87 | 1154640 | 65 | blastx.14 | (AF112206) ras-related
protein rab-14 [Homo
sapiens]
GTP-binding protein | gb AAF17194.1 AF1
12206_1
gi 409166 gb AAA34 | 100%
96% | 851
99 | 219
254 |

| | | | | | | | | |
|---------|---------|-----|----------------------------|--|---|-----------------------------|---------------------------|---------------------------|
| HDTJF87 | 907527 | 488 | HMMER
2.1.1
blastx.2 | [Volvox carteri]
PFAM: Ras family | 253.1
PF00071 | 198.2 | 110 | 394 |
| HE8TB94 | 1178794 | 66 | blastx.14 | strong similarity to the
YPT1 sub-family of RAS
proteins [Caenorhabditis
elegans] | gb AAB52431.1 | 97%
73% | 89
396 | 394
737 |
| HE8TB94 | 935935 | 489 | HMMER
2.1.1
blastx.2 | ras-like protein [Homo
sapiens]
PFAM: Ras family | gi 190881 gb AAA36
547.1
PF00071 | 78%
78%
236.3 | 527
507
529 | 1075
548
1104 |
| HE8UB55 | 912932 | 490 | HMMER
1.8
blastx.2 | ras-like protein [Homo
sapiens]
PFAM: Ras family
(contains ATP/GTP
binding P-loop) | gb AAA36547.1
PF00071 | 80%
271.56 | 523
197 | 1101
676 |
| HEBGA65 | 1178633 | 68 | blastx.14 | (AL049685) hypothetical
protein [Homo sapiens]
Rab24 protein [Mus
musculus] | emb CAB41256.1
gi 438164 emb CAA8
0472.1
PF00071 | 89%
90%
94%
176.38 | 185
435
1076
451 | 688
860
1252
939 |
| HEBGA65 | 912815 | 491 | HMMER
1.8
blastx.2 | PFAM: Ras family
(contains ATP/GTP
binding P-loop)
Rab24 protein [Mus
musculus] | emb CAA80472.1 | 92% | 442 | 1035 |
| HEGBB59 | 1197907 | 69 | blastx.14 | RAS-LIKE PROTEIN
RASD
(TRANSFORMING
PROTEIN P23). | sp P03967 RASD_DI
CDI | 47%
57%
53% | 671
497
944 | 928
679
988 |
| HEGBB59 | 912601 | 492 | HMMER
1.8 | PFAM: Ras family
(contains ATP/GTP) | PF00071 | 75.96 | 370 | 546 |

| | | | | | blastx.2 | binding P-loop)
ras protein [Suberites
domuncula] | emb CAA77070.1 | | | |
|---------|---------|-----|--|--|--------------|---|---|------------|------------|------------|
| HELHC48 | 956003 | 70 | | | HMMER
1.8 | PFAM: Ras family
(contains ATP/GTP
binding P-loop) | PF00071 | 156.24 | 756 | 403 |
| | | | | | blastx.2 | (AF106681) ras-related
GTP-binding protein
[Homo sapiens] | gb AAD43034.1 | 96%
76% | 756
817 | 403
767 |
| HEOQH90 | 1212646 | 71 | | | blastx.14 | GTPase Rab37. | sp AAF67162 AAF67
162 | 93% | 12 | 680 |
| HEOQH90 | 907532 | 493 | | | HMMER
1.8 | PFAM: Ras family
(contains ATP/GTP
binding P-loop) | PF00071 | 305.73 | 88 | 666 |
| | | | | | blastx.2 | (AB027137) RAB-26
[Homo sapiens] | dbj BAA84707.1 | 72% | 94 | 657 |
| HFKHA18 | 1152242 | 72 | | | blastx.14 | (AF058807) GTP-binding
protein rah [Bos taurus] | gi 4587775 gb AAD2
5874.1 | 97%
95% | 94
427 | 426
690 |
| HFKHA18 | 972414 | 494 | | | HMMER
1.8 | PFAM: Ras family
(contains ATP/GTP
binding P-loop) | PF00071 | 142.21 | 91 | 408 |
| | | | | | blastx.2 | (AF058807) GTP-binding
protein rah [Bos taurus] | gb AAD25874.1 | 97%
93% | 88
409 | 420
684 |
| HFKMA10 | 964258 | 73 | | | HMMER
1.8 | PFAM: Ras family
(contains ATP/GTP
binding P-loop) | PF00071 | 254.6 | 254 | 721 |
| | | | | | blastx.2 | Rab22a protein [Canis
familiaris] | emb CAA80473.1 | 99% | 242 | 724 |
| HHBFM91 | 1092116 | 74 | | | blastx.14 | (AF091035) GTP-binding
protein RAB21 [Homo
sapiens] | gi 6002585 gb AAF00
048.1 AF091035_1 | 100% | 3 | 479 |

| | | | | | | | | |
|---------|---------|-----|----------------|---|-------------------------------|--------|-----|-----|
| HHBFM91 | 912832 | 495 | HMMER
1.8 | PFAM: Ras family
(contains ATP/GTP
binding P-loop) | PF00071 | 86.13 | 2 | 340 |
| | | | blastx.2 | (AF091035) GTP-binding
protein RAB21 [Homo
sapiens] | gb AAF00048.1 AF0
91035_1 | 97% | 2 | 316 |
| HIBBF63 | 912715 | 75 | HMMER
2.1.1 | PFAM: Ras family | PF00071 | 211.1 | 3 | 416 |
| | | | blastx.2 | (AB027137) RAB-26
[Homo sapiens] | dbj BAA84707.1 | 100% | 3 | 419 |
| HMCEI38 | 1134410 | 76 | blastx.14 | (AF081353) GTP-binding
protein [Homo sapiens] | gi 3859936 gb AAC7
2918.1 | 81% | 229 | 594 |
| HMCEI38 | 912580 | 496 | HMMER
2.1.1 | PFAM: Ras family | PF00071 | 103.6 | 297 | 452 |
| | | | blastx.2 | (AF081353) GTP-binding
protein [Homo sapiens] | gb AAC72918.1 | 81% | 228 | 593 |
| HMWJD68 | 1154790 | 77 | blastx.14 | (AK000254) unnamed
protein product [Homo
sapiens] | gi 7020212 dbj BAA9
1034.1 | 98% | 54 | 614 |
| HMWJD68 | 912628 | 497 | HMMER
2.1.1 | PFAM: Ras family | PF00071 | 231.3 | 113 | 685 |
| | | | blastx.2 | (AK000254) unnamed
protein product [Homo
sapiens] | dbj BAA91034.1 | 99% | 53 | 613 |
| HOEOL58 | 1078090 | 78 | blastx.14 | small GTP-binding
protein Rab27b [Homo
sapiens] | gi 5107835 gb AAC5
1194.2 | 100% | 102 | 338 |
| HOEOL58 | 912836 | 498 | HMMER
1.8 | PFAM: Ras family
(contains ATP/GTP
binding P-loop) | PF00071 | 150.75 | 3 | 407 |
| | | | blastx.2 | small GTP-binding | gb AAC51194.2 | 97% | 3 | 407 |

| | | | | | | | | |
|---------|---------|-----|-------------------------|--|--|--|--|---|
| HRACA51 | 1162856 | 79 | blastx.14 | protein Rab27b [Homo sapiens]
rab4b [Canis familiaris] | gi 919 emb CAA39800.1 | 100% | 54 | 677 |
| HRACA51 | 912776 | 499 | HMMER 2.1.1
blastx.2 | PFAM: Ras family | PF000071 | 310.6 | 55 | 666 |
| HSHAV32 | 912812 | 500 | HMMER 1.8
blastx.2 | rab4b [Canis familiaris]
PFAM: Ras family
(contains ATP/GTP binding P-loop) | emb CAA39800.1
PF000071 | 100%
242.77 | 43
192 | 666
872 |
| HTPDE66 | 971281 | 81 | blastx.2
HMMER 1.8 | (AB034244) RAB23
protein [Homo sapiens]
PFAM: Ras family
(contains ATP/GTP binding P-loop) | dbj BAA87324.1
PF000071 | 99%
73.53 | 162
260 | 872
427 |
| HTPDV73 | 997659 | 82 | blastx.2 | small GTP-binding protein [Oryctolagus cuniculus]
N-methyl-D-aspartate receptor subunit [Rattus rattus] | gb AAA31261.1
gi 286238 dbj BAA02500.1 | 100%
63%
66%
30%
70%
71%
83%
85%
71% | 260
216
39
123
5
290
123
248
331 | 427
281
74
182
34
310
140
268
351 |
| HTPDV73 | 912947 | 501 | HMMER 1.8
blastx.2 | PFAM: Ras family
(contains ATP/GTP binding P-loop)
(AL049685) hypothetical protein [Homo sapiens] | PF000071
emb CAB41256.1 | 205.32
97% | 306
312 | 740
746 |
| HTPHE33 | 963658 | 502 | HMMER | PFAM: Ras family | PF000071 | 94.19 | 993 | 1433 |

| | | | | | | | | |
|---------|---------|-------------|---|--------------------------|-------------------|-------------------|-------------------|--|
| | | 1.8 | (contains ATP/GTP binding P-loop) | | | | | |
| | | blastx.2 | (AF095350) RAB-like protein 2A [Homo sapiens] | gb AAD51377.1 AF095350_1 | 83%
93% | 993
793 | 1478
1014 | |
| HUFDN58 | 1224609 | blastx.14 | RAS-LIKE PROTEIN RASD (TRANSFORMING PROTEIN P23). | sp P03967 RASD_DI CDI | 47%
57%
53% | 664
490
937 | 921
672
981 | |
| HUFDN58 | 912929 | HMMER 2.1.1 | PFAM: Ras family | PF00071 | 80.7 | 42 | 296 | |
| | | blastx.2 | ras-related protein [Dictyostelium discoideum] | emb CAA78508.1 | 43% | 3 | 299 | |
| HUVFX92 | 1225329 | blastx.14 | GTP-binding protein ypt1 [similarity] - Neurospora crassa | pir S30096 S30096 | 88% | 54 | 308 | |
| HUVFX92 | 912672 | HMMER 2.1.1 | PFAM: Ras family | PF00071 | 161 | 81 | 278 | |
| | | blastx.2 | (AF101310) similar to RAS-related proteins; contains similarity 1 | gb AAC69218.1 | 100% | 54 | 275 | |
| HWAEG71 | 1182321 | blastx.14 | rab-related GTP-binding protein [Rattus norvegicus] | gi 206543 gb AAA42000.1 | 96% | 85 | 690 | |
| HWAEG71 | 931547 | HMMER 1.8 | PFAM: Ras family (contains ATP/GTP binding P-loop) | PF00071 | 147.95 | 116 | 475 | |
| | | blastx.2 | rab-related GTP-binding protein [Rattus norvegicus] | gb AAA42000.1 | 98%
80% | 86
477 | 493
569 | |

| | | | | | | | | |
|----------|---------|-----|----------------|--|-----------------------------|--------------------------|------------------------|--------------------------|
| HW AHD49 | 1228064 | 87 | blastx.14 | GTP-BINDING
PROTEIN RAH
(FRAGMENT). | sp Q9XS71 Q9XS71 | 97%
94% | 391
742 | 747
1011 |
| HW AHD49 | 972413 | 506 | HMMER
1.8 | PFAM: Ras family
(contains ATP/GTP
binding P-loop) | PF00071 | 143.42 | 394 | 717 |
| | | | blastx.2 | LMW G-protein=low-
molecular-weight GTP-
binding protein [mice,
HT4 neural cell line,
Peptide, 208 aa] [Mus sp.] | gb AAB20669.1 | 95%
76% | 391
726 | 720
764 |
| HW LGG31 | 1178825 | 88 | blastx.14 | RAB15 [Rattus
norvegicus] | gi 206537 gb AAA41
995.1 | 92% | 81 | 716 |
| HW LGG31 | 912581 | 507 | HMMER
2.1.1 | PFAM: Ras family | PF00071 | 301.8 | 98 | 562 |
| | | | blastx.2 | RAB15 [Rattus
norvegicus] | gb AAA41995.1 | 90% | 71 | 562 |
| HW LKF25 | 912842 | 508 | HMMER
2.1.1 | PFAM: Ras family | PF00071 | 298.2 | 311 | 889 |
| | | | blastx.2 | (AB036693) RAB9-like
protein [Homo sapiens] | dbj BAA89542.1 | 100% | 287 | 889 |
| H2CBH45 | 963811 | 90 | HMMER
1.8 | PFAM: Src homology
domain 3 | PF00018 | 13 | 194 | 310 |
| | | | blastx.2 | Kryn [Mus musculus] | dbj BAA19686.1 | 85%
79%
87%
70% | 2
381
460
131 | 373
467
483
160 |
| HAGDN53 | 895963 | 509 | HMMER
1.8 | PFAM: Src homology
domain 3 | PF00018 | 22.95 | 270 | 335 |
| | | | blastx.2 | coded for by C. elegans
cDNA yk34a9.5; coded | gb AAA96115.1 | 43%
38% | 165
103 | 455
156 |

| | | | | for by C. elegans 1
elegans] | | | | | |
|---------|---------|-----|----------------|---|------------------------------|---------------------------|-------------------------|--------------------------|--|
| HAMFM39 | 971347 | 92 | HMMER
1.8 | PFAM: Src homology
domain 3 | PF00018 | 67.14 | 1136 | 1306 | |
| | | | blastx.2 | (AK001509) unnamed
protein product [Homo
sapiens] | dbj BAA91729.1 | 59% | 4511 | 4017 | |
| HBGQT03 | 908173 | 93 | HMMER
2.1.1 | PFAM: SH3 domain | PF00018 | 68.5 | 615 | 785 | |
| | | | blastx.2 | (AF130979) SH3 domain-
containing protein 6511
[Homo sapiens] | gb AAF04472.1 AF1
30979_1 | 93% | 3 | 791 | |
| HBGSJ13 | 1150790 | 94 | blastx.14 | ferrienterobactin receptor .
precursor [Escherichia
coli] | gi 1778500 gb AAB4
0783.1 | 93% | 729 | 1 | |
| HBGSJ13 | 878322 | 510 | HMMER
1.8 | PFAM: Src homology
domain 3 | PF00018 | 4.07 | 445 | 510 | |
| | | | blastx.2 | ferrienterobactin receptor
precursor [Escherichia
coli] | gb AAB40783.1 | 92% | 64 | 684 | |
| HBIBQ89 | 909782 | 95 | HMMER
2.1.1 | PFAM: SH3 domain | PF00018 | 49.7 | 212 | 376 | |
| | | | blastx.2 | p115 [Homo sapiens] | emb CAA55394.1 | 41% | 14 | 397 | |
| HCECM90 | 945088 | 96 | HMMER
1.8 | PFAM: Src homology
domain 3 | PF00018 | 53.06 | 392 | 568 | |
| HCEPH71 | 522739 | 97 | HMMER
1.8 | PFAM: Src homology
domain 3 | PF00018 | 4.22 | 33 | 62 | |
| HCFMT57 | 1175204 | 98 | blastx.14 | (AF039571) peripheral
benzodiazepine receptor
interacting protein; PBR-
IP/PRAX1 [Homo | gi 4104812 gb AAD1
1957.1 | 96%
74%
100%
52% | 45
702
887
381 | 629
887
979
500 | |

| | | | | | | | | | | |
|---------|---------|-----|--------------|---|-----------------------------|--|-------|-----|------|------|
| | | | | | sapiens] | | | 44% | 381 | 461 |
| | | | | | | | | 55% | 327 | 386 |
| | | | | | | | | 28% | 161 | 319 |
| | | | | | | | | 50% | 744 | 803 |
| | | | | | | | | 58% | 780 | 830 |
| | | | | | | | | 35% | 160 | 243 |
| | | | | | | | | 34% | 1693 | 1770 |
| | | | | | | | | 47% | 468 | 518 |
| | | | | | | | | 55% | 190 | 243 |
| | | | | | | | | 58% | 795 | 830 |
| | | | | | | | | 42% | 622 | 684 |
| | | | | | | | | 29% | 73 | 153 |
| | | | | | | | | 42% | 607 | 663 |
| | | | | | | | | 35% | 54 | 137 |
| | | | | | | | | 36% | 643 | 717 |
| | | | | | | | | 31% | 631 | 717 |
| | | | | | | | | 25% | 136 | 231 |
| | | | | | | | | 38% | 111 | 188 |
| | | | | | | | | 28% | 114 | 230 |
| | | | | | | | | 28% | 144 | 227 |
| HCFMT57 | 765375 | 511 | HMMER
1.8 | PFAM: Src homology
domain 3 | PF00018 | | 14.55 | 107 | 3 | |
| | | | blastx.2 | (AF039571) peripheral
benzodiazepine receptor
interacting protein; PBR-
IP/PRAX1 [Homo
sapiens] | gb AAD11957.1 | | 96% | 377 | 3 | |
| HCOMM05 | 1173146 | 99 | blastx.14 | epidermal growth factor
receptor kinase substrate
[Homo sapiens] | gi 530823 gb AAA62
280.1 | | 44% | 456 | 722 | |
| | | | | | | | 59% | 189 | 371 | |
| | | | | | | | 46% | 723 | 851 | |
| | | | | | | | 23% | 54 | 233 | |
| | | | | | | | 36% | 126 | 191 | |

| | | | | | | | | |
|---------|--------|-----|----------------------------|---|---|-----------------------------------|--------------------------------|---------------------------------|
| HCOMM05 | 925952 | 512 | HMMER
1.8
blastx.2 | PFAM: Src homology
domain 3
epidermal growth factor
receptor kinase substrate
[Homo sapiens] | PF00018 | 63% | 1081 | 1113 |
| HCOOZ11 | 965306 | 100 | HMMER
1.8
blastx.2 | PFAM: Src homology
domain 3
(AL022238) dJ1042K10.2
(supported by
GENSCAN, FGENES and
GENEWISE) [Homo
sapiens] | gb AAA62280.1
PF00018
emb CAA18266.1 | 46%
43%
23%
5.22
100% | 445
115
43
179
182 | 840
435
222
214
589 |
| HCWFF88 | 506577 | 101 | HMMER
1.8 | PFAM: Src homology
domain 3 | PF00018 | 4.92 | 140 | 181 |
| HDMAV01 | 911386 | 513 | HMMER
1.8
blastx.2 | PFAM: Src homology
domain 3
unnamed protein product
[unidentified] | PF00018
emb CAB42388.1 | 52.13
73%
100% | 264
111
3 | 413
410
116 |
| HDPDA47 | 929193 | 103 | HMMER
1.8
blastx.2 | PFAM: Src homology
domain 3
(AL049683) hypothetical
protein [Homo sapiens] | PF00018
emb CAB41255.1 | 12.52
69% | 691
145 | 810
1026 |
| HDPFF24 | 909232 | 104 | HMMER
2.1.1
blastx.2 | PFAM: KRAB box
(AC007228) R31665_2
[AA 1-673] [Homo
sapiens] | PF01352
gb AAD23606.1 AC0
07228_1 | 53%
121.3
50% | 945
158
158 | 1022
349
457 |
| HDPPO35 | 966248 | 105 | HMMER
1.8
blastx.2 | PFAM: Src homology
domain 3
(AL049683) hypothetical | PF00018
emb CAB41255.1 | 14.07
39% | 600
84 | 749
1148 |

| | | | | | | | | |
|---------|---------|-----|--------------------------|--|--|--|--|---|
| HDPSR74 | 911396 | 106 | HMMER
1.8
blastx.2 | protein [Homo sapiens]
PFAM: Src homology
domain 3
(AF104246) enhancer of
filamentation 1 homolog
[Gallus gallus] | PF00018 | 47.19 | 293 | 460 |
| HDTKQ14 | 886936 | 107 | HMMER
1.8
blastx.2 | PFAM: Src homology
domain 3
(AL049683) hypothetical
protein [Homo sapiens] | PF00018 | 12.87 | 430 | 546 |
| HE6GF02 | 1150897 | 108 | blastx.14 | (AJ007012) Fish protein
[Mus musculus] | emb[CAB41255.1]
gi 3702174 emb CAA
07416.1 | 100%
56%
75%
66%
70%
39%
40%
38%
39%
41%
38%
37%
37%
50%
54% | 439
76
795
603
189
603
804
792
795
600
582
552
150
532
459 | 555
291
613
427
70
430
613
637
637
427
433
481
70
485
427 |
| HE6GF02 | 911263 | 514 | HMMER
1.8
blastx.2 | PFAM: Src homology
domain 3
(AJ007012) Fish protein
[Mus musculus] | PF00018 | 51.15 | 10 | 174 |
| HE8PK12 | 909884 | 109 | HMMER
1.8
blastx.2 | PFAM: Src homology
domain 3
(AF136380) SH3P12
protein [Homo sapiens] | emb CAA07416.1
PF00018 | 77%
44%
58.12 | 10
201
197 | 186
275
361 |
| HE9SE62 | 911476 | 110 | HMMER | PFAM: Src homology | gi AAD27647.1 AF1
36380_1
PF00018 | 82%
47.65 | 59
268 | 367
435 |

| | | | | | | | | | |
|---------|--------|-----|----------|--|----------------|-------|------|------|--|
| | | | 1.8 | domain 3 | | | | | |
| | | | blastx.2 | (AK000007) FLJ00007 protein [Homo sapiens] | dbj BAA92232.1 | 43% | 4 | 435 | |
| | | | 1.8 | PFAM: Src homology domain 3 | PF00018 | 64% | 877 | 927 | |
| HEOPL36 | 968826 | 515 | HMMER | (AL049758) dJ437M21.3 (protein kinase C and casein kinase substrate in neurons 2) [Homo sapiens] | emb CAB51395.1 | 79.81 | 316 | 483 | |
| | | | blastx.2 | | | 99% | 178 | 486 | |
| HFBDJ13 | 911264 | 112 | HMMER | PFAM: SH3 domain | PF00018 | 78.6 | 105 | 269 | |
| | | | 2.1.1 | | | | | | |
| | | | blastx.2 | (AF030131) Plenty of SH3s; POSH [Mus musculus] | gb AAC40070.1 | 78% | 3 | 473 | |
| HFTDF15 | 657020 | 113 | HMMER | PFAM: Src homology domain 3 | PF00018 | 4.85 | 168 | 203 | |
| | | | 1.8 | | | | | | |
| HHEQV39 | 932851 | 114 | HMMER | PFAM: Src homology domain 3 | PF00018 | 30.41 | 526 | 708 | |
| | | | 1.8 | | | | | | |
| HHFCK09 | 965304 | 115 | HMMER | PFAM: TBC domain | PF00566 | 179.1 | 2305 | 1655 | |
| | | | 2.1.1 | | | | | | |
| | | | blastx.2 | (AL022238) dJ1042K10.2 (supported by GENSCAN, FGENES and GENEWISE) [Homo sapiens] | emb CAA18266.1 | 97% | 2635 | 1268 | |
| | | | | | | 98% | 1276 | 389 | |
| HISDS62 | 935932 | 116 | HMMER | PFAM: RhoGEF domain | PF00621 | 51.3 | 229 | 486 | |
| | | | 2.1.1 | | | | | | |
| | | | blastx.2 | (AJ250425) Collybistin I [Rattus norvegicus] | emb CAB65966.1 | 96% | 1 | 483 | |
| HLQDT35 | 839777 | 117 | HMMER | PFAM: Src homology | PF00018 | 3.85 | 342 | 419 | |

| | | | | | | | | |
|---------|--------|-----|--------------------------|--|------------------------------|---------------------------------|---------------------------|---------------------------------|
| | | | 1.8
blastx.2 | domain 3
(AK000579) unnamed
protein product [Homo
sapiens] | dbj BAA91269.1 | 98% | 252 | 458 |
| HLWFN63 | 908437 | 118 | HMMER
1.8
blastx.2 | PFAM: Src homology
domain 3
(AL049683) hypothetical
protein [Homo sapiens] | PF00018 | 12.81 | 515 | 664 |
| HMEFT66 | 856149 | 119 | HMMER
1.8 | PFAM: Src homology
domain 3 | emb CAB41255.1 | 44% | 464 | 1024 |
| HMSCD15 | 918133 | 120 | HMMER
1.8
blastx.2 | PFAM: Src homology
domain 3
(AK000975) unnamed
protein product [Homo
sapiens] | PF00018 | 28.51 | 5 | 136 |
| HMSHO64 | 746582 | 121 | HMMER
1.8
blastx.2 | PFAM: Src homology
domain 3
(AF030131) Plenty of
SH3s; POSH [Mus
musculus] | dbj BAA91451.1 | 98%
29%
28% | 453
387
80 | 635
479
175 |
| HMTAW83 | 911385 | 122 | HMMER
1.8
blastx.2 | PFAM: Src homology
domain 3
(AF230904) c-Cbl-
interacting protein [Homo
sapiens] | PF00018 | 11.08 | 316 | 405 |
| HMVAM09 | 963814 | 123 | HMMER
1.8
blastx.2 | PFAM: Src homology
domain 3
(AK001580) unnamed
protein product [Homo
sapiens] | gb AAF37854.1 AF2
30904_1 | 47%
76.18 | 1 | 159 |
| | | | | | | 94%
52%
48%
61%
75% | 1
7
7
298
425 | 354
210
168
351
460 |
| | | | | | | 4.79 | 728 | 802 |
| | | | | | | 96% | 20 | 802 |

| | | | | | | | | |
|---------|---------|-----|----------------------------|--|---|------------|-----------|------------|
| HNSAA28 | 946988 | 124 | HMMER
2.1.1
blastx.2 | sapiens]
PFAM: SH3 domain | PF00018 | 149 | 757 | 915 |
| | | | | (AF146277) adapter
protein CMS [Homo
sapiens] | gb AAD34595.1 AF1
46277_1 | 82% | 4 | 1554 |
| HNSAA28 | 972348 | 516 | blastx.14 | (AF146277) adapter
protein CMS [Homo
sapiens] | gi 4960047 gb AAD3
4595.1 AF146277_1 | 88% | 21 | 449 |
| HOGEQ43 | 935465 | 517 | HMMER
1.8
blastx.2 | PFAM: Src homology
domain 3 | PF00018 | 28.13 | 58 | 132 |
| | | | | (AF132480) Ese2 protein
[Mus musculus] | gb AAD19748.1 | 93% | 37 | 132 |
| HOUDH19 | 1150918 | 126 | blastx.14 | (AC007842) BC331191_1
[Homo sapiens] | gi 5080758 gb AAD3
9268.1 AC007842_3 | 91% | 350 | 27 |
| HOUDH19 | 908588 | 518 | HMMER
2.1.1
blastx.2 | PFAM: KRAB box | PF01352 | 169.7 | 241 | 429 |
| | | | | (AC007842) BC331191_1
[Homo sapiens] | gb AAD39268.1 AC0
07842_3 | 91% | 226 | 549 |
| HOUFT36 | 911293 | 127 | HMMER
2.1.1
blastx.2 | PFAM: PDZ domain
(Also known as DHR or
GLGF) | PF00595 | 35.3 | 322 | 558 |
| | | | | (AF162130) MAGUK
protein TEM-61 [Homo
sapiens] | gb AAD45919.2 AF1
62130_1 | 91%
98% | 196
23 | 846
193 |
| HPMFL08 | 959569 | 128 | HMMER
1.8 | PFAM: Src homology
domain 3 | PF00018 | 4.97 | 209 | 238 |
| HRSMD49 | 723025 | 129 | HMMER
1.8 | PFAM: Src homology
domain 3 | PF00018 | 4.76 | 199 | 270 |
| HSDII69 | 917180 | 130 | HMMER
1.8 | PFAM: Src homology
domain 3 | PF00018 | 4.09 | 382 | 429 |

| | | | | | | | | |
|---------|--------|-----|----------------------------|---|----------------|------------|----------|------------|
| HSDSB06 | 949151 | 131 | HMMER
2.1.1
blastx.2 | PFAM: SH3 domain
(AL133047) hypothetical
protein [Homo sapiens] | PF00018 | 249.3 | 483 | 647 |
| HSFAM09 | 573345 | 519 | HMMER
1.8 | PFAM: Src homology
domain 3 | PF00018 | 5.33 | 195 | 218 |
| HSSAX53 | 507509 | 133 | HMMER
1.8 | PFAM: Src homology
domain 3 | PF00018 | 4.36 | 266 | 331 |
| HSVAV49 | 689674 | 520 | HMMER
1.8
blastx.2 | PFAM: Src homology
domain 3
(AF146277) adapter
protein CMS [Homo
sapiens] | PF00018 | 36.33 | 77 | 169 |
| HTEAG49 | 954614 | 135 | HMMER
1.8 | PFAM: Src homology
domain 3 | PF00018 | 4.51 | 312 | 238 |
| HTLBH67 | 751985 | 136 | HMMER
1.8 | PFAM: Src homology
domain 3 | PF00018 | 37.78 | 16 | 162 |
| HTLJC71 | 922923 | 137 | HMMER
1.8
blastx.2 | PFAM: Src homology
domain 3
(AL133030) hypothetical
protein [Homo sapiens] | PF00018 | 9.14 | 1152 | 1340 |
| HTPAD46 | 503313 | 138 | HMMER
1.8 | PFAM: Src homology
domain 3 | emb CAB61362.1 | 94% | 3 | 1355 |
| HTTKP07 | 911390 | 139 | HMMER
1.8
blastx.2 | PFAM: Src homology
domain 3
(AL049683) hypothetical
protein [Homo sapiens] | PF00018 | 4.14 | 160 | 186 |
| HUCOW17 | 933357 | 140 | HMMER
1.8
blastx.2 | PFAM: Src homology
domain 3
Graf protein [Homo | PF00018 | 15.82 | 47 | 196 |
| | | | | | emb CAB41255.1 | 51%
56% | 8
292 | 289
450 |
| | | | | | PF00018 | 20.28 | 647 | 739 |
| | | | | | emb CAA71414.2 | 67% | 1 | 261 |

| | | | | | | | | |
|---------|---------|-----|--------------------------|--|---|---------------------------|--------------------------|--------------------------|
| HWHGF52 | 726102 | 141 | HMMER
1.8
blastx.2 | sapiens]
PFAM: Src homology
domain 3
Dbs=Dbl guanine
nucleotide exchange
factor homolog [mice,
32D 1 | PF00018
gb AAB33461.1 | 50%
83%
40%
5.01 | 608
756
187
325 | 751
809
246
387 |
| HWHHB69 | 690442 | 521 | HMMER
1.8
blastx.2 | PFAM: Src homology
domain 3
(AF178432) SH3 protein
[Homo sapiens] | PF00018
gb AAF35985.1 AF1
78432.1 | 31.65
70%
100% | 91
91
303 | 255
315
329 |
| HWLFH94 | 1151387 | 143 | blastx.14 | (AK000265) unnamed
protein product [Homo
sapiens] | gi 7020230 dbj BAA9
1041.1 | 41%
53%
52% | 545
689
949 | 345
594
887 |
| HWLFH94 | 909682 | 522 | HMMER
1.8
blastx.2 | PFAM: Src homology
domain 3
(AK000265) unnamed
protein product [Homo
sapiens] | PF00018
dbj BAA91041.1 | 58.42
40% | 308
215 | 463
535 |
| HWMBM13 | 909683 | 144 | HMMER
1.8
blastx.2 | PFAM: Src homology
domain 3
Eps8 [Mus musculus] | PF00018
gb AAA16358.1 | 59.64
35%
37% | 126
33
324 | 281
317
527 |
| HWWDN34 | 911357 | 145 | HMMER
1.8
blastx.2 | PFAM: Src homology
domain 3
(AF053130)
unconventional myosin
MYO15 [Mus musculus] | PF00018
gb AAC40124.1 | 14.09
42%
66% | 686
56
788 | 853
874
868 |
| HCEML27 | 771667 | 523 | HMMER | PFAM: Src homology | PF00017 | 42.63 | 14 | 202 |

| | | | 1.8 | domain 2 | | | | |
|----------|---------|-----|-----------------------|--|-------------------------------------|--|---------------------------------------|---|
| | | | blastx.2 | (AL049924) hypothetical protein [Homo sapiens] | emb CAB43208.1 | 88% | 2 | 322 |
| HELHJ69 | 1128924 | 147 | blastx.14 | (AF124251) SH2-containing protein Nsp3 [Homo sapiens] | gi 4704739 gb AAD28246.1 AF124251_1 | 81%
76%
52%
60%
63% | 66
586
590
55
612 | 593
624
640
99
644 |
| HELHJ69 | 911262 | 524 | HMMER 1.8
blastx.2 | PFAM: Src homology domain 2
(AF124251) SH2-containing protein Nsp3 [Homo sapiens] | PF00017 | 72.59 | 241 | 483 |
| HFKLA09 | 952634 | 525 | HMMER 2.1.1 | PFAM: Src homology domain 2 | PF00017 | 46.9 | 758 | 1036 |
| HSBBF79 | 965764 | 149 | HMMER 1.8 | PFAM: Src homology domain 2 | PF00017 | 69.47 | 384 | 614 |
| HSLKA77 | 911589 | 526 | HMMER 1.8
blastx.2 | PFAM: Src homology domain 2
tensin [Gallus gallus] | PF00017
gb AAA49087.1 | 37.25 | 301 | 405 |
| hagdr21 | 1090433 | 151 | blastx.14 | p66shc [Homo sapiens] | gi 1899055 gb AAB49972.1 | 58%
51%
31% | 178
29
3 | 432
115
155 |
| hagdr21 | 1002124 | 527 | blastx.14 | MUS p66 Shc [Mus musculus] | gi 1200456 gb AAA91777.1 | 69%
72%
59%
37%
35%
34% | 848
134
380
665
72
701 | 1150
412
475
751
164
778 |
| HHFNIH27 | 1025277 | 152 | blastx.2 | collagen alpha 1(III) chain | pir S05272 CGHU7L | 91%
30% | 62
89 | 268
1609 |

HTLIT05 1217625 153 blastx.14 CDNA FLJ10243 FIS,
CLONE
HEMBB1000631,
WEAKLY SIMILAR TO
1

| | | | | | | | | |
|---------|---------|-----|-----------|--|--------------------------|-----|------|------|
| HTLIT05 | 1217625 | 153 | blastx.14 | CDNA FLJ10243 FIS,
CLONE
HEMBB1000631,
WEAKLY SIMILAR TO
1 | sp BAA91505 BAA9
1505 | 31% | 1656 | 835 |
| | | | | | | 32% | 1848 | 952 |
| | | | | | | 29% | 1662 | 955 |
| | | | | | | 36% | 525 | 55 |
| | | | | | | 37% | 525 | 19 |
| | | | | | | 32% | 525 | 37 |
| | | | | | | 33% | 1659 | 1063 |
| | | | | | | 30% | 1656 | 1021 |
| | | | | | | 30% | 1644 | 958 |
| | | | | | | 32% | 642 | 64 |
| | | | | | | 34% | 534 | 85 |
| | | | | | | 33% | 592 | 11 |
| | | | | | | 30% | 654 | 7 |
| | | | | | | 39% | 226 | 8 |
| | | | | | | 28% | 598 | 2 |
| | | | | | | 30% | 648 | 85 |
| | | | | | | 41% | 229 | 11 |
| | | | | | | 30% | 589 | 17 |
| | | | | | | 37% | 211 | 11 |
| | | | | | | 34% | 226 | 23 |
| | | | | | | 33% | 250 | 11 |
| | | | | | | 35% | 226 | 23 |
| | | | | | | 43% | 190 | 11 |
| | | | | | | 36% | 259 | 41 |
| | | | | | | 44% | 125 | 45 |
| | | | | | | 52% | 128 | 72 |
| HTLIT05 | | | | | | 49% | 213 | 584 |
| HTLIT05 | 1095161 | 528 | blastx.14 | (AK001105) unnamed | gi 7022161 dbj BAA9 | 49% | 212 | 577 |

| | | | | | | | | |
|----------|---------|-----|-------------------------|---|--------------------------------------|---------------|-----------|------------|
| HAPNV33 | 1151374 | 154 | blastx.14 | protein product [Homo sapiens]
(AK001267) unnamed protein product [Homo sapiens] | 1505.1
gi 7022415 dbj BAA91590.1 | 100% | 1 | 774 |
| HAPNV33 | 947872 | 529 | HMMER 1.8
blastx.14 | PFAM: ATPases associated with various cellular activities (AAA)
(AF016427) Contains similarity to Pfam domain: 1 elegans] | PF00004
gi 2291232 gb AAB65351.1 | 120.31
53% | 61
1 | 450
447 |
| HBTAEE84 | 1128800 | 155 | blastx.14 | ATP-dependent Clp protease ATP-binding subunit ClpA.
[Escherichia coli] | gi 1651401 dbj BAA35601.1 | 100% | 3 | 299 |
| HBTAEE84 | 781946 | 530 | HMMER 1.8 | PFAM: ATPases associated with various cellular activities (AAA) | PF00004 | 20.81 | 122 | 232 |
| HDPVY89 | 827026 | 156 | HMMER 2.1.1 | PFAM: ATPases associated with various cellular activities (AAA) | PF00004 | 30.6 | 431 | 490 |
| HGLDB21 | 455474 | 531 | HMMER 1.8 | PFAM: ATPases associated with various cellular activities (AAA) | PF00004 | 19.89 | 12 | 80 |
| HMIAN37 | 947881 | 158 | HMMER 2.1.1
blastx.2 | PFAM: ATPases associated with various cellular activities (AAA)
Similarity to Yeast MSP1 protein (TAT-binding homolog 4)
(SW:MSP1_YEAST) [Caenorhabditis elegans] | PF00004
emb CAA93516.1 | 109
45% | 436
91 | 642
642 |

| HODAK55 | 745532 | 532 | HMMER
1.8 | PFAM: ATPases
associated with various
cellular activities (AAA) | PF00004 | 60.69 | 11 | 157 |
|---------|---------|-----|--------------|--|---|--------------------------|----------------------|-------------------------|
| HSLEI59 | 1128801 | 160 | blastx.14 | ATP-dependent Clp
protease ATP-binding
subunit ClpA.
[Escherichia coli] | gi 1651401 dbj BAA3
5601.1 | 94% | 3 | 770 |
| HSLEI59 | 781945 | 533 | HMMER
1.8 | PFAM: ATPases
associated with various
cellular activities (AAA) | PF00004 | 20.14 | 96 | 206 |
| HSQFH29 | 1217061 | 161 | blastx.14 | SPAF. | sp Q9Z2K7 Q9Z2K7 | 89%
52%
36% | 101
5
854 | 1723
208
961 |
| HSQFH29 | 967708 | 534 | HMMER
1.8 | PFAM: ATPases
associated with various
cellular activities (AAA) | PF00004 | 97.36 | 193 | 393 |
| HTLEA35 | 1107230 | 162 | blastx.14 | (AF049099) SPAF [Mus
musculus] | gi 4105619 gb AAD0
2481.1 | 83%
43%
76%
61% | 70
76
408
3 | 417
414
470
41 |
| HTLEA35 | 827028 | 535 | HMMER
1.8 | (AK001571) unnamed
protein product [Homo
sapiens] | gi 7022907 dbj BAA9
1764.1 | 100% | 3 | 479 |
| HUVGG63 | 969432 | 536 | HMMER
1.8 | PFAM: ATPases
associated with various
cellular activities (AAA) | PF00004 | 332.15 | 621 | 1178 |
| HAGAX57 | 1150865 | 164 | blastx.14 | PFAM: ATPases
associated with various
cellular activities (AAA) | gi 5732691 gb AAD4
9227.1 AF159063.1 | 97% | 138 | 1448 |
| | | | | homolog [Homo sapiens] | gi 5815353 gb AAD5 | 100% | 192 | 785 |
| | | | | (AF176012) J domain | | | | |

| | | | | | | | | |
|---------|---------|-----|-----------------------------|---|--|--|--|--|
| HAGAX57 | 949211 | 537 | HMMER
1.8
blastx.14 | containing protein 1
isoform a [Homo sapiens]
PFAM: DnaJ, prokaryotic
heat shock protein.
(AF176012) J domain
containing protein 1
isoform a [Homo sapiens]
(AL032657) predicted
using Genefinder; similar
to 111 ES | 2650.1 AF176012_1
PF00226
gi 5815353 gb AAD5
2650.1 AF176012_1
gi 3881075 emb CAA
21734.1 | 67.6
100%
64%
52%
66%
32%
45%
26% | 224
185
335
560
665
623
674
626 | 421
778
565
667
736
733
733
751 |
| HAMGX15 | 1177932 | 165 | blastx.14 | | | 80.1 | 554 | 709 |
| HAMGX15 | 908840 | 538 | HMMER
2.1.1
blastx.14 | PFAM: DnaJ domain
(AL032657) predicted
using Genefinder; similar
to 111 ES | PF00226
gi 3881075 emb CAA
21734.1 | 51% | 506 | 715 |
| HAUBV06 | 1106041 | 166 | blastx.14 | similar to [SwissProt
Accession Number
P08409]; 1 | gi 1799806 dbj BAA1
6264.1 | 98%
80% | 1164
2104 | 2120
2166 |
| HAUBV06 | 596802 | 539 | HMMER
2.1.1 | PFAM: DnaJ C terminal
region | PF01556 | 262.1 | 567 | 932 |
| HAUBV06 | 929762 | 540 | HMMER
2.1.1 | PFAM: DnaJ C terminal
region | PF01556 | 249.7 | 1650 | 1285 |
| HBWCM62 | 908818 | 541 | HMMER
1.8
blastx.14 | PFAM: DnaJ, prokaryotic
heat shock protein
contains strong similarity
to a DnaJ-like domain
(PS:PS00636)
[Caenorhabditis elegans] | PF00226
gi 1707079 gb AAB3
7835.1 | 97.9
42% | 37
19 | 243
306 |

| | | | | | | | | |
|---------|---------|-----|-------------|---|-------------------------------------|--------|-----|-----|
| HCWFA35 | 1105672 | 168 | blastx.14 | Curved DNA-binding protein cbpA [Escherichia coli] | gi 1651491 dbj BAA36142.1 | 98% | 68 | 322 |
| HCWFA35 | 908820 | 542 | HMMER 1.8 | PFAM: DnaJ, prokaryotic heat shock protein | PF00226 | 116.61 | 80 | 274 |
| | | | blastx.14 | Curved DNA-binding protein cbpA [Escherichia coli] | gi 1651491 dbj BAA36142.1 | 98% | 68 | 364 |
| HDACA35 | 1107236 | 169 | blastx.14 | (AK001496) unnamed protein product [Homo sapiens] | gi 7022789 dbj BAA91724.1 | 76% | 71 | 904 |
| HDACA35 | 908837 | 543 | HMMER 1.8 | PFAM: DnaJ, prokaryotic heat shock protein | PF00226 | 65.68 | 68 | 229 |
| | | | blastx.14 | cysteine string protein [Bos taurus] | gi 1232165 emb CAA63355.1 | 49% | 80 | 256 |
| HDQGM08 | 1151469 | 170 | blastx.14 | (AF176013) J domain containing protein 1 isoform b [Homo sapiens] | gi 5815355 gb AAD52651.1 AF176013_1 | 100% | 37 | 357 |
| HDQGM08 | 949210 | 544 | HMMER 1.8 | PFAM: DnaJ, prokaryotic heat shock protein | PF00226 | 68.48 | 466 | 269 |
| | | | blastx.14 | (AF176013) J domain containing protein 1 isoform b [Homo sapiens] | gi 5815355 gb AAD52651.1 AF176013_1 | 100% | 505 | 185 |
| HELGB06 | 1148741 | 171 | blastx.14 | ORF-1 [Escherichia coli] | gi 402674 gb AAA18299.1 | 100% | 248 | 3 |
| HELGB06 | 935730 | 545 | HMMER 2.1.1 | PFAM: DnaJ domain | PF00226 | 78.3 | 203 | 421 |
| | | | blastx.14 | ORF-1 [Escherichia coli] | gi 402674 gb AAA18299.1 | 100% | 200 | 445 |
| HEOPR74 | 908836 | 546 | HMMER 1.8 | PFAM: DnaJ, prokaryotic heat shock protein | PF00226 | 88.67 | 65 | 262 |

| | | | | | | | | |
|---------|---------|-----|-----------------------------|--|-------------------------------|--------------------------|-------------------------|---------------------------|
| HIBEK35 | 731480 | 173 | blastx.14
HMMER
2.1.1 | cysteine string protein
[Bos taurus] | gi 1232163 emb CAA
63354.1 | 41% | 68
457 | 289
492 |
| HJMAR88 | 908839 | 547 | blastx.14
HMMER
2.1.1 | PFAM: DnaJ domain | PF00226 | 112.7 | 237 | 404 |
| HMWGU56 | 908825 | 548 | blastx.14
HMMER
2.1.1 | PFAM: DnaJ domain | PF00226 | 42.7 | 57 | 149 |
| | | | blastx.14 | cysteine string protein 1 -
human | pir S70515 S70515 | 68%
100% | 6
1 | 254
60 |
| | | | blastx.14 | PFAM: DnaJ domain | PF00226 | 126.9 | 375 | 569 |
| | | | blastx.14 | Similarity to B.subtilis
DNAJ protein 1
[Caenorhabditis elegans] | gi 3873707 emb CAA
97416.1 | 59%
65%
34% | 327
630
51 | 587
698
200 |
| HOUDS09 | 1164010 | 176 | blastx.14 | (AK000034) unnamed
protein product [Homo
sapiens] | gi 7019854 dbj BAA9
0896.1 | 66%
35%
45%
32% | 240
729
96
174 | 659
1118
167
248 |
| HOUDS09 | 949051 | 549 | HMMER
1.8 | PFAM: DnaJ, prokaryotic
heat shock protein | PF00226 | 98.53 | 310 | 504 |
| | | | blastx.2 | (AK000034) unnamed
protein product [Homo
sapiens] | dbj BAA90896.1 | 53%
55%
63% | 37
899
2 | 888
1033
34 |
| HTEGM38 | 675087 | 177 | HMMER
2.1.1 | PFAM: DnaJ domain | PF00226 | 65.2 | 93 | 197 |
| HTEKY82 | 908846 | 550 | HMMER
2.1.1 | PFAM: DnaJ domain | PF00226 | 119.6 | 281 | 475 |
| | | | blastx.14 | Similarity to B.subtilis
DNAJ protein 1
[Caenorhabditis elegans] | gi 3873707 emb CAA
97416.1 | 53% | 236 | 502 |
| HTLCY54 | 1193550 | 179 | blastx.14 | MDJ6. | sp Q9QY17 Q9QY17 | 94%
81% | 239
796 | 460
927 |

| | | | | | | | | |
|---------|--------|-----|-----------------------------|---|-------------------------------------|--------------------------|------------------------|--------------------------|
| HTLCY54 | 908832 | 551 | HMMER
2.1.1
blastx.14 | PFAM: DnaJ domain
(AB014888) MRJ [Homo sapiens] | PF00226 | 81%
73%
119.8 | 484
610
245 | 597
699
445 |
| HFOXK14 | 603245 | 180 | HMMER
1.8 | PFAM: Adenylate and Guanylate cyclase catalytic domain | PF00211 | 137.85 | 183 | 401 |
| HHFFO69 | 837703 | 181 | HMMER
1.8 | PFAM: Adenylate and Guanylate cyclase catalytic domain | PF00211 | 386.54 | 124 | 708 |
| HHFLU06 | 857884 | 182 | HMMER
2.1.1 | PFAM: Adenylate and Guanylate cyclase catalytic domain | PF00211 | 108.8 | 17 | 268 |
| HAGBA56 | 732597 | 183 | HMMER
2.1.1 | PFAM: Eukaryotic protein kinase domain | PF00069 | 64.9 | 139 | 516 |
| HAGGF84 | 911312 | 184 | HMMER
1.8
blastx.14 | PFAM: Eukaryotic protein kinase domain
calmodulin-dependent protein kinase II-delta dash [Oryctolagus cuniculus] | PF00069 | 105.85 | 10 | 318 |
| HAHGD33 | 921782 | 185 | HMMER
1.8
blastx.14 | PFAM: Eukaryotic protein kinase domain
(AF145690)
BcDNA.LD28657 [Drosophila melanogaster] | PF00069 | 83.68 | 4 | 564 |
| | | | | | gi 3241849 dbj BAA28870.1 | 88%
87%
100% | 10
366
320 | 363
413
364 |
| | | | | | gi 5052670 gb AAD38665.1 AF145690_1 | 68%
56%
60%
39% | 1
412
304
676 | 297
609
426
804 |

| | | | | | | | | |
|---------|--------|-----|-----------------------------|---|---|-------|-----|-----|
| HAHIY08 | 962113 | 186 | HMMER
1.8
blastx.14 | PFAM: Eukaryotic protein
kinase domain
similar to tyrosine kinase
[Caenorhabditis elegans] | PF000069
gi 470364 gb AAC47
047.1 | 74.92 | 39 | 278 |
| HBIOZ10 | 973131 | 187 | HMMER
1.8
blastx.2 | PFAM: Eukaryotic protein
kinase domain
(AF003134) strong
similarity to the
CDC2/CDX subfamily of
ser/thr protein kinases
[Caenorhabditis elegans] | PF000069
gb AAB54139.1 | 121.1 | 3 | 365 |
| HBKDI30 | 729048 | 188 | HMMER
1.8 | PFAM: Eukaryotic protein
kinase domain | PF000069 | 42.23 | 1 | 213 |
| HBXBW40 | 706115 | 189 | HMMER
1.8 | PFAM: Eukaryotic protein
kinase domain | PF000069 | 34.01 | 280 | 423 |
| HCEHE35 | 909937 | 190 | HMMER
1.8
blastx.14 | PFAM: Eukaryotic protein
kinase domain
protein kinase PRK2
[human, DX3 B-cell
myeloma cell line,
Peptide, 984 aa] [Homo
sapiens] | PF000069
gi 914100 gb AAB33
346.1 | 30.78 | 210 | 347 |
| HCEPW85 | 911374 | 191 | HMMER
1.8
blastx.14 | PFAM: Eukaryotic protein
kinase domain
predicted using
Genefinder; Similarity to
111 cDNA | PF000069
gi 3875903 emb CAA
94127.1 | 66% | 204 | 365 |
| HCFAT25 | 932068 | 192 | HMMER
2.1.1
blastx.14 | PFAM: Eukaryotic protein
kinase domain
(AF096300) HPK/GCK- | PF000069
gi 4322936 gb AAD1 | 83.52 | 3 | 260 |
| | | | | | | 87% | 3 | 260 |
| | | | | | | 26.6 | 136 | 231 |
| | | | | | | 63% | 91 | 456 |

| | | | | | | | | |
|---------|---------|-----|-----------------------------|--|--|----------------------------|------------------------|---------------------------|
| HCFCF47 | 1139731 | 193 | blastx.14 | like kinase HGK [Homo sapiens]
(AF003134) strong similarity to the CDC2/CDX 1 | 6137.1] | 72%
25% | 60
232 | 158
312 |
| HCFCF47 | 894415 | 552 | HMMER
1.8 | PFAM: Eukaryotic protein kinase domain | PF00069 | 89.54 | 20 | 295 |
| HDAAV61 | 810305 | 194 | HMMER
1.8 | PFAM: Eukaryotic protein kinase domain | PF00069 | 41.11 | 11 | 145 |
| HDPKD75 | 810824 | 195 | HMMER
1.8 | PFAM: Eukaryotic protein kinase domain | PF00069 | 98.74 | 68 | 433 |
| HDPNC96 | 934520 | 196 | HMMER
1.8 | PFAM: Eukaryotic protein kinase domain | PF00069 | 206.63 | 3 | 734 |
| HDPSR15 | 969666 | 197 | HMMER
1.8
blastx.2 | HUMAN NDR [unidentified]
PFAM: Eukaryotic protein kinase domain
(AB026289) protein kinase SID6-1512 [Homo sapiens] | gi 2304746 emb CAA03387.1]
PF00069
dbj BAA85045.1] | 92%
87.19
95%
89% | 3
351
631
240 | 734
626
1158
692 |
| HDQDX20 | 919027 | 198 | HMMER
2.1.1
blastx.14 | PFAM: PX domain
serine/threonine protein kinase [Rattus norvegicus] | PF00787
gi 294637 gb AAA42137.1] | 73.4
78%
44% | 246
633
465 | 569
974
578 |
| HDQHB19 | 895106 | 553 | HMMER
2.1.1 | PFAM: Eukaryotic protein kinase domain | PF00069 | 92.5 | 260 | 520 |
| HDTBY88 | 934472 | 200 | HMMER
2.1.1
blastx.14 | PFAM: Eukaryotic protein kinase domain
p56 KIAMRE protein kinase [Homo sapiens] | PF00069
gi 1517820 gb AAC50918.1] | 93.6
82%
35% | 3
3
192 | 302
170
458 |

| | | | | | | | | |
|---------|--------|-----|----------------------------|---|-------------------------------|-------------------|-----------------|-------------------|
| HE2KZ07 | 909948 | 201 | HMMER
1.8
blastx.14 | PFAM: Eukaryotic protein
kinase domain
(AB004267)
Ca2+/calmodulin-
dependent protein kinase I
beta 2 [Rattus norvegicus] | gi 3135197 dbj BAA2
8263.1 | 100% | 492 | 509 |
| HE8UY74 | 960914 | 202 | HMMER
1.8
blastx.14 | PFAM: Eukaryotic protein
kinase domain
(AF080119) contains
similarity to protein
kinase 1 | gi 3600036 gb AAC3
5524.1 | 36.37% | 114 | 407 |
| HE9NO66 | 974353 | 203 | HMMER
1.8
blastx.14 | PFAM: Eukaryotic protein
kinase domain
(AB020741) NIK-related
kinase [Mus musculus] | gi 6009519 dbj BAA8
4943.1 | 73%
94%
79% | 449
2
748 | 817
283
990 |
| HEMBT61 | 939957 | 204 | HMMER
2.1.1
blastx.2 | PFAM: Eukaryotic protein
kinase domain
(AD000092) hypothetical
human serine-threonine
protein kinase R31240_1
[Homo sapiens] | gb AAB51171.1 | 76.6% | 16 | 285 |
| HETLF29 | 909762 | 205 | HMMER
1.8
blastx.14 | PFAM: Eukaryotic protein
kinase domain
similar to cAMP-
dependant protein kinase;
cDNA EST 111 | gi 3878636 emb CAA
88953.1 | 71% | 13 | 441 |
| HFIUE75 | 909758 | 206 | HMMER
1.8 | PFAM: Eukaryotic protein
kinase domain | PF00069 | 143.18% | 6 | 416 |
| | | | | | | 56% | 6 | 416 |
| | | | | | PF00069 | 85.68% | 377 | 664 |

| | | | | | | | | |
|---------|--------|-----|-------------|---|-------------------------------------|------------|------------|------------|
| | | | blastx.14 | (AD000092) hypothetical human serine-threonine protein kinase R31240_1 [Homo sapiens] | gi 1905906 gb AAB51171.1 | 43% | 362 | 634 |
| HFKIT06 | 934019 | 207 | HMMER 1.8 | PFAM: Eukaryotic protein kinase domain | PF000069 | 34.65 | 160 | 270 |
| | | | blastx.14 | p58 galactosyltransferase-associated protein kinase - human | pir A38282 A38282 | 51%
40% | 178
74 | 270
118 |
| HHEGC20 | 894409 | 208 | HMMER 1.8 | PFAM: Eukaryotic protein kinase domain | PF000069 | 200.01 | 26 | 598 |
| HHEHC53 | 921783 | 209 | HMMER 1.8 | PFAM: Eukaryotic protein kinase domain | PF000069 | 58.81 | 507 | 797 |
| | | | blastx.14 | (AF145690) BcDNA.LD28657 [Drosophila melanogaster] | gi 5052670 gb AAD38665.1 AF145690_1 | 79%
70% | 567
321 | 803
563 |
| HHERQ79 | 944057 | 210 | HMMER 1.8 | PFAM: Eukaryotic protein kinase domain | PF000069 | 83.4 | 133 | 474 |
| | | | blastx.2 | (AB016589) inducible IKappaB kinase [Mus musculus] | dbj BAA85154.1 | 90% | 109 | 471 |
| HISAF59 | 959140 | 211 | HMMER 1.8 | PFAM: Eukaryotic protein kinase domain | PF000069 | 89.46 | 340 | 771 |
| | | | blastx.14 | (AC002343) Ser/Thr protein kinase isolog [Arabidopsis thaliana] | gi 2262107 gb AAB63615.1 | 39%
33% | 460
397 | 768
468 |
| HKAKM10 | 918685 | 212 | HMMER 2.1.1 | PFAM: Eukaryotic protein kinase domain | PF000069 | 31.4 | 8 | 127 |
| HLTHP86 | 919354 | 213 | HMMER 2.1.1 | PFAM: TBC domain | PF00566 | 69.4 | 855 | 1274 |
| | | | blastx.2 | (AF161420) HSPC302 | gb AAF28980.1 AF1 | 89% | 456 | 1352 |

| | | | | | | | | |
|---------|--------|-----|--------------|---|---|--|---|--|
| HMSJL96 | 934483 | 214 | HMMER
1.8 | [Homo sapiens]
PFAM: Eukaryotic protein
kinase domain | 61420_1
PF000069 | 99%
52% | 1309
1253 | 1974
1309 |
| HMTAJ73 | 813296 | 215 | HMMER
1.8 | PFAM: Eukaryotic protein
kinase domain | PF000069 | 26.49
21.34 | 199
4 | 363
114 |
| HNTCP13 | 909770 | 216 | HMMER
1.8 | PFAM: Eukaryotic protein
kinase domain | PF000069 | 102.96 | 445 | 930 |
| HNTMD79 | 934522 | 217 | blastx.14 | (AC006530) unknown
[Homo sapiens] | gi 4809337 gb AAD3
0182.1 AC006530_4 | 55% | 463 | 957 |
| | | | HMMER
1.8 | PFAM: Eukaryotic protein
kinase domain | PF000069 | 130.82 | 203 | 586 |
| HNTMH70 | 757184 | 218 | blastx.14 | LATS [Drosophila
melanogaster] | gi 903942 gb AAA70
336.1 | 52%
33%
57%
22% | 239
76
169
64 | 586
156
210
240 |
| | | | HMMER
1.8 | PFAM: Eukaryotic protein
kinase domain | PF000069 | 94.55 | 176 | 577 |
| HNTNB14 | 909942 | 219 | HMMER
1.8 | PFAM: Eukaryotic protein
kinase domain | PF000069 | 96.28 | 38 | 343 |
| | | | blastx.14 | calmodulin-binding
protein [Rattus
norvegicus] | gi 349075 gb AAA16
633.1 | 97%
85%
74%
77%
69%
65%
60%
52%
37%
39%
35%
33% | 41
553
553
553
559
553
553
553
553
553
553
559 | 475
657
657
657
657
657
657
654
657
636
645
657 |

| | | | | | | | | |
|---------|--------|-----|----------------------------|--|------------------------------|----------------------------------|--------------------------------|---------------------------------|
| HODFF88 | 974911 | 220 | HMMER
1.8
blastx.14 | PFAM: Eukaryotic protein
kinase domain
mixed-lineage protein
kinase 1 - human | PF00069
pir S32467 JU0229 | 77%
29%
101.43 | 512
556
98 | 538
657
370 |
| HOHCE47 | 911566 | 554 | HMMER
1.8 | PFAM: Eukaryotic protein
kinase domain | PF00069 | 79.42 | 211 | 423 |
| HPCR84 | 945856 | 222 | HMMER
1.8
blastx.2 | PFAM: Eukaryotic protein
kinase domain
similar to protein kinase
of X.laavis, has putative 1 | PF00069
dbj BAA11492.1 | 75.57
78% | 157
127 | 384
483 |
| HRACK83 | 888037 | 223 | HMMER
1.8 | PFAM: Eukaryotic protein
kinase domain | PF00069 | 48.4 | 211 | 423 |
| HRADM45 | 717358 | 224 | HMMER
1.8
blastx.2 | PFAM: Eukaryotic protein
kinase domain
(AJ271722) putative
serine/threonine protein
kinase MAK-V [Homo
sapiens] | PF00069
emb CAB71146.1 | 23.7
98% | 14
2 | 124
469 |
| HRAED74 | 942527 | 225 | HMMER
1.8
blastx.2 | PFAM: Eukaryotic protein
kinase domain
(AB023658)
Ca/calmodulin-dependent
protein kinase kinase
alpha, CaM-kinase kinase
alpha [Rattus norvegicus] | PF00069
dbj BAA75246.1 | 59.6
97%
81%
71%
88% | 406
71
388
342
662 | 612
346
648
425
688 |
| HRDZ70 | 942673 | 226 | HMMER
2.1.1
blastx.2 | PFAM: Eukaryotic protein
kinase domain
kinase like protein | PF00069
emb CAB10257.1 | 78.2
39% | 33
33 | 248
323 |

| | | | | | | | | |
|---------|---------|-----|-----------------------------|---|---|----------------------------------|------------------------------|----------------------------------|
| HSKAC24 | 823869 | 227 | HMMER
1.8 | [Arabidopsis thaliana]
PFAM: Eukaryotic protein
kinase domain | PF000069 | 50% | 303 | 380 |
| HSSMT34 | 911294 | 228 | HMMER
1.8 | PFAM: Eukaryotic protein
kinase domain | PF000069 | 53.16 | 95 | 292 |
| HT3BG12 | 921593 | 229 | HMMER
1.8 | PFAM: Eukaryotic protein
kinase domain | PF000069 | 27.09 | 109 | 183 |
| | | | blastx.14 | CYCLIN-DEPENDENT
KINASE (CDK)8
[unidentified] | gi 3715669 emb CAA
03585.1 | 85% | 1 | 246 |
| HTEGO05 | 932583 | 230 | HMMER
2.1.1
blastx.14 | PFAM: Eukaryotic protein
kinase domain
male germ cell-associated
kinase (mak) [Rattus
norvegicus] | PF000069
gi 205278 gb AAA41
562.1 | 50.8
85%
64%
85%
38% | 3
3
489
768
1023 | 233
395
761
848
1100 |
| HTEKT33 | 953308 | 231 | HMMER
1.8
blastx.2 | PFAM: Eukaryotic protein
kinase domain
(AC007661) putative
protein kinase
[Arabidopsis thaliana] | PF000069
gb AAD32787.1 AC0
07661_24 | 200.58
41%
36%
29% | 428
722
1070
428 | 1393
1009
1243
628 |
| HTEMU66 | 944419 | 232 | HMMER
1.8
blastx.2 | PFAM: Eukaryotic protein
kinase domain
MEK Kinase 3 [Mus
musculus] | PF000069
gb AAB03355.1 | 114.85
49%
29% | 613
604
209 | 963
948
340 |
| HTEMV09 | 909843 | 233 | HMMER
1.8
blastx.14 | PFAM: Eukaryotic protein
kinase domain
protein kinase I [Rattus
norvegicus] | PF000069
gi 406113 gb AAA19
670.1 | 99.16
44% | 19
1 | 312
321 |
| HTEMV66 | 1151075 | 234 | blastx.14 | contains EGF-like repeats;
highly similar to ZC84.1; | gi 495684 gb AAA50
735.1 | 55%
44% | 579
783 | 223
649 |

| | | | | | | | | | |
|---------|---------|-----|-----------------------------|---|---|---|--------------------------|--------------------------|--------------------------|
| HTMV66 | 813038 | 555 | HMMER
2.1.1 | 1 | PFAM: Eukaryotic protein
kinase domain | PF00069 | 23% | 861 | 772 |
| HTGAU79 | 1175071 | 235 | blastx.14 | | (AL157917) similarity to
endopeptidases 1 | gi 7106102 emb CAB
76028.1 | 50%
38%
60%
52% | 755
371
641
323 | 976
571
730
373 |
| HTGAU79 | 940369 | 556 | HMMER
1.8
blastx.2 | | PFAM: Eukaryotic protein
kinase domain | PF00069 | 31.25 | 315 | 779 |
| HTLEJ11 | 973302 | 236 | HMMER
2.1.1
blastx.14 | | (AL157917) similarity to
endopeptidases
[Schizosaccharomyces 1
PFAM: Eukaryotic protein
kinase domain | emb CAB76028.1
PF00069 | 45%
55.9 | 324
44 | 977
223 |
| HTLIY52 | 1218691 | 237 | blastx.14 | | (AF144573) Mx-
interacting protein kinase
PKM [Mesocricetus
auratus] | gi 4868443 gb AAD3
1319.1 AF144573_1 | 69%
40%
42%
38% | 35
437
293
877 | 268
592
397
939 |
| HTLIY52 | 942161 | 557 | HMMER
1.8
blastx.2 | | TESTIS-SPECIFIC
SERINE/THREONINE
KINASE. | sp Q61241 Q61241 | 46%
48%
45%
42% | 640
142
427
565 | 972
414
579
621 |
| HTOAK34 | 966800 | 238 | HMMER
1.8
blastx.14 | | PFAM: Eukaryotic protein
kinase domain | PF00069 | 251.19 | 166 | 933 |
| | | | | | serine/threonine kinase
[Mus musculus] | gb AAA99535.1 | 44% | 133 | 936 |
| | | | | | PFAM: Eukaryotic protein
kinase domain | PF00069 | 32.41 | 1020 | 1190 |
| | | | | | (AF084205)
serine/threonine protein
kinase TAO1 [Rattus | gi 3452473 gb AAC7
1014.1 | 75% | 954 | 1190 |

| | | | | | | | | |
|---------|---------|-----|---------------------------|---|---|---|--|--|
| HTPGG25 | 911282 | 239 | HMMER
1.8
blastx.2 | norvegicus]
PFAM: Eukaryotic protein
kinase domain
(AL117482) hypothetical
protein [Homo sapiens] | PF00069 | 114.02 | 72 | 353 |
| HUJAD24 | 1161319 | 240 | blastx.14 | serine/threonine kinase
[Rattus norvegicus] | gi 2052191 emb CAB
06295.1 | 34%
48%
34%
57%
48%
24%
47%
72%
42% | 439
345
779
267
123
57
3
211
162 | 759
494
910
344
215
206
53
243
218 |
| HUJAD24 | 911498 | 558 | HMMER
1.8
blastx.14 | PFAM: Eukaryotic protein
kinase domain
AMP-activated protein
kinase homolog [Homo
sapiens] | PF00069 | 34.73 | 9 | 215 |
| HUTSF11 | 966029 | 241 | HMMER
1.8
blastx.14 | PFAM: Eukaryotic protein
kinase domain
PRO1038. | PF00069 | 27.74 | 3 | 104 |
| HUVGZ88 | 1227628 | 242 | blastx.14 | kinase domain | sp AAF71042 AAF71
042 | 59%
41%
39%
75% | 425
1159
1282
1695 | 859
1296
1404
1742 |
| HUVGZ88 | 959020 | 559 | HMMER
1.8
blastx.14 | PFAM: Eukaryotic protein
kinase domain
(AF191838) TANK
binding kinase TBK1 | PF00069 | 31.12 | 182 | 439 |
| HWADY66 | 1096252 | 243 | blastx.14 | | gi 6224868 gb AAF05
989.1 AF191838.1 | 84% | 10 | 183 |

| | | | | | | | | |
|---------|---------|-----|----------------|---|---|--------------------------|------------------------------|-----------------------------|
| HWADY66 | 734565 | 560 | HMMER
1.8 | [Homo sapiens]
PFAM: Eukaryotic protein
kinase domain | PF00069 | 28.82 | 1 | 174 |
| HWAFG04 | 952878 | 244 | HMMER
1.8 | PFAM: Eukaryotic protein
kinase domain | PF00069 | 93.74 | 1655 | 945 |
| | | | blastx.14 | (AC002343) Ser/Thr
protein kinase isolog
[Arabidopsis thaliana] | gi 2262107 gb AAB6
3615.1 | 41%
48%
42%
75% | 1655
1319
1046
1355 | 1383
1185
933
1332 |
| HWAFS18 | 948434 | 245 | HMMER
1.8 | PFAM: Eukaryotic protein
kinase domain | PF00069 | 115.98 | 225 | 632 |
| | | | blastx.14 | (AF156884) RIP-like
kinase [Homo sapiens] | gi 5059425 gb AAD3
9005.1 AF156884_1 | 91%
66%
100% | 165
702
632 | 632
773
661 |
| HWAGS73 | 1150212 | 246 | blastx.14 | (AF156884) RIP-like
kinase [Homo sapiens] | gi 5059425 gb AAD3
9005.1 AF156884_1 | 82% | 1 | 273 |
| HWAGS73 | 894404 | 561 | HMMER
1.8 | PFAM: Eukaryotic protein
kinase domain | PF00069 | 64.17 | 4 | 273 |
| HWLEA48 | 927676 | 247 | HMMER
1.8 | PFAM: Eukaryotic protein
kinase domain | PF00069 | 32.82 | 190 | 381 |
| | | | blastx.2 | (AF169034) protein
kinase [Homo sapiens] | gb AAF12757.2 AF1
69034_1 | 59%
100%
51% | 154
89
287 | 429
166
415 |
| HWLHS82 | 934505 | 248 | HMMER
2.1.1 | PFAM: Eukaryotic protein
kinase domain | PF00069 | 147.2 | 2 | 319 |
| | | | blastx.2 | (AC005581) R31237_1,
partial CDS [Homo
sapiens] | gb AAC33487.1 | 90%
100%
40% | 68
2
306 | 364
76
422 |
| HWMIB81 | 955336 | 249 | HMMER
1.8 | PFAM: Eukaryotic protein
kinase domain | PF00069 | 122.85 | 1458 | 934 |
| | | | blastx.2 | (AK000528) unnamed | dbj BAA91232.1 | 100% | 3 | 572 |

| | | | | | | | | |
|---------|---------|-----|--------------------------|---|--|--------------------------|----------------------------|----------------------------|
| HCWDV17 | 1105673 | 250 | blastx.14 | protein product [Homo sapiens]
BvgA positive transcription regulator (put.); putative [Bordetella pertussis] | gi 144039 gb AAA22969.1 | 57%
70% | 203
77 | 604
187 |
| HCWDV17 | 974478 | 562 | HMMER 1.8 | PFAM: Bacterial regulatory proteins, luxR family | PF00196 | 81.59 | 416 | 613 |
| HELDI95 | 1103374 | 251 | blastx.14 | Regulatory protein KdpD. [Escherichia coli] | gi 1651302 dbj BAA3532.1 | 100% | 103 | 525 |
| HELDI95 | 953059 | 563 | HMMER 1.8
blastx.14 | PFAM: Response regulator receiver domain | PF00072 | 123.84 | 482 | 766 |
| HAGFO25 | 1150845 | 252 | blastx.14 | Regulatory protein KdpD. [Escherichia coli] | gi 1651302 dbj BAA3532.1 | 98% | 1 | 432 |
| HAGFO25 | 957992 | 564 | HMMER 1.8
blastx.14 | (AF062595) adenylylate kinase 5 [Homo sapiens]
PFAM: Adenylylate kinases | gi 4691541 gb AAD27956.1 AF062595_1
PF00406 | 92%
206.82 | 145
180 | 732
650 |
| HAWAB54 | 1149319 | 253 | blastx.14 | (AF062595) adenylylate kinase 5 [Homo sapiens] | gi 4691541 gb AAD27956.1 AF062595_1 | 90%
92%
30%
29% | 135
876
1341
1413 | 728
283
1012
1321 |
| HAWAB54 | 957993 | 565 | HMMER 2.1.1
blastx.14 | PFAM: Adenylylate kinase | PF00406 | 40.1 | 111 | 296 |
| HLIBV06 | 934887 | 254 | HMMER 2.1.1
blastx.14 | (AF062595) adenylylate kinase 5 [Homo sapiens]
PFAM: Adenylylate kinase | gi 4691541 gb AAD27956.1 AF062595_1
PF00406 | 98%
100.8 | 111
81 | 374
245 |
| | | | | (AB020203) adenylylate | gi 4760600 dbj BAA7 | 90% | 81 | 350 |

| | | | | | | | | |
|---------|---------|-----|-------------|---|------------------------------|-------|-----|------|
| HMALL66 | 1105097 | 255 | blastx.14 | kinase isozyme 3 [Mus musculus]
adenylate kinase (EC 2.7.4.3), chloroplast - maize | 7360.1
pir S45634 S45634 | 45% | 71 | 292 |
| HMALL66 | 956195 | 566 | HMMER 1.8 | PFAM: Adenylate kinases | PF00406 | 50.17 | 63 | 296 |
| HOACE12 | 858976 | 256 | HMMER 2.1.1 | PFAM: Adenylate kinase | PF00406 | 46.1 | 20 | 235 |
| HOGCG69 | 924848 | 257 | HMMER 1.8 | PFAM: Adenylate kinases | PF00406 | 76.14 | 858 | 1145 |
| HAGAE09 | 525926 | 567 | blastx.14 | adenylate kinase (EC 2.7.4.3), chloroplast - maize | pir S45634 S45634 | 36% | 480 | 791 |
| | | | | | | 35% | 849 | 1145 |
| | | | | | | 33% | 379 | 522 |
| | | | | | | 57% | 214 | 255 |
| HAGAE09 | 525926 | 567 | HMMER 1.8 | PFAM: Phorbol esters / diacylglycerol binding domain | PF00130 | 3.93 | 159 | 185 |
| HAGAE34 | 525878 | 568 | HMMER 1.8 | PFAM: Phorbol esters / diacylglycerol binding domain | PF00130 | 8.88 | 191 | 253 |
| HARMH78 | 1137572 | 260 | blastx.14 | (AF001435) unknown [Homo sapiens] | gi 2529709 gb AAB81205.1 | 32% | 237 | 395 |
| | | | | | | 43% | 135 | 203 |
| | | | | | | 75% | 482 | 505 |
| HARMH78 | 773210 | 569 | HMMER 1.8 | PFAM: Phorbol esters / diacylglycerol binding domain | PF00130 | 4.88 | 192 | 227 |
| HBJLB53 | 974122 | 570 | HMMER 1.8 | PFAM: Phorbol esters / diacylglycerol binding domain | PF00130 | 4.62 | 301 | 348 |
| HBJNB52 | 726475 | 571 | HMMER | PFAM: Phorbol esters / | PF00130 | 3.77 | 193 | 252 |

| | | | | 1.8 | diacylglycerol binding domain | | | | |
|---------|---------|-----|--|-----------|--|---------------------------|-------------------|---------------------|---------------------|
| HDABQ83 | 669619 | 572 | | HMMER 1.8 | PFAM: Phorbol esters / diacylglycerol binding domain | PF00130 | 6.04 | 255 | 284 |
| HDPDC84 | 616980 | 573 | | HMMER 1.8 | PFAM: Phorbol esters / diacylglycerol binding domain | PF00130 | 25.6 | 253 | 393 |
| HDPUF40 | 1212494 | 265 | | blastx.14 | PTPL1-ASSOCIATED RHOGAP. | sp O15463 O15463 | 54%
46%
23% | 286
1018
1537 | 867
1230
1662 |
| HDPUF40 | 970586 | 574 | | HMMER 1.8 | PFAM: Phorbol esters / diacylglycerol binding domain | PF00130 | 26.42 | 415 | 546 |
| | | | | blastx.14 | similar to C.elegans protein (Z37093) [Homo sapiens] | gi 1504026 dbj BAA13212.1 | 94%
98% | 61
654 | 651
806 |
| HDPWU07 | 952734 | 575 | | HMMER 1.8 | PFAM: Phorbol esters / diacylglycerol binding domain | PF00130 | 2.94 | 333 | 356 |
| HDTJJ02 | 913787 | 576 | | HMMER 1.8 | PFAM: Phorbol esters / diacylglycerol binding domain | PF00130 | 5.7 | 21 | 68 |
| HE2GA18 | 1121872 | 268 | | blastx.14 | mhpR [Escherichia coli] | gi 1702880 emb CAA70746.1 | 98% | 288 | 1 |
| HE2GA18 | 867276 | 577 | | HMMER 1.8 | PFAM: Phorbol esters / diacylglycerol binding domain | PF00130 | 4.09 | 74 | 109 |
| HE2SY03 | 947947 | 578 | | HMMER 1.8 | PFAM: Phorbol esters / diacylglycerol binding domain | PF00130 | 2.97 | 387 | 437 |

| | | | | | | | | |
|---------|---------|-----|-----------|--|-------------------------------------|-------------------|-------------------|------------------|
| HELGY64 | 934511 | 579 | blastx.14 | (AF118023) SH3 domain-binding protein SNP70 [Homo sapiens]
PFAM: Phorbol esters / diacylglycerol binding domain | gi 4836401 gb AAD30425.1 AF118023_1 | 46% | 456 | 301 |
| HF1YW31 | 697730 | 580 | HMMER 1.8 | PFAM: Phorbol esters / diacylglycerol binding domain | PF00130 | 76.38 | 241 | 390 |
| HFVIP88 | 960741 | 581 | HMMER 1.8 | PFAM: Phorbol esters / diacylglycerol binding domain | PF00130 | 3.29 | 29 | 67 |
| HGBAS76 | 771320 | 582 | HMMER 1.8 | PFAM: Phorbol esters / diacylglycerol binding domain | PF00130 | 7.32 | 147 | 206 |
| HHEBB62 | 1151481 | 274 | blastx.14 | (AK000193) unnamed protein product [Homo sapiens] | gi 7020117 dbj BAA91000.1 | 100% | 1 | 375 |
| HHEBB62 | 791469 | 583 | HMMER 1.8 | PFAM: Phorbol esters / diacylglycerol binding domain | PF00130 | 6.2 | 292 | 236 |
| HHEHU73 | 923895 | 584 | HMMER 1.8 | PFAM: Phorbol esters / diacylglycerol binding domain | PF00130 | 4.1 | 115 | 156 |
| HHEMA11 | 966924 | 585 | HMMER 1.8 | PFAM: Phorbol esters / diacylglycerol binding domain | PF00130 | 10.16 | 354 | 395 |
| HHEQK01 | 1107392 | 277 | blastx.14 | ORF 3 [Homo sapiens] | gi 182221 gb AA58464.1 | 37%
55%
39% | 165
266
342 | 22
213
274 |
| HHEQK01 | 871911 | 586 | HMMER 1.8 | PFAM: Phorbol esters / diacylglycerol binding domain | PF00130 | 3.27 | 64 | 90 |

| | | | | | | | | |
|----------|---------|-----|----------------|--|-------------------------------|--|---|--|
| HHP84 | 915639 | 278 | HMMER
1.8 | domain
PFAM: Phorbol esters /
diacylglycerol binding
domain | PF00130 | 12.35 | 146 | 187 |
| HHSED84 | 706739 | 587 | HMMER
2.1.1 | PFAM: Sterol O-
acyltransferase | PF01800 | 276.4 | 2 | 364 |
| HIBCC94 | 504326 | 588 | HMMER
1.8 | PFAM: Phorbol esters /
diacylglycerol binding
domain | PF00130 | 3.12 | 177 | 206 |
| HKADN56 | 1220254 | 281 | blastx.14 | CG5276 PROTEIN. | sp Q9VGN8 Q9VGN8 | 58%
68%
54%
43%
63%
47%
87%
42% | 904
1465
1279
796
754
706
1627
102 | 1257
1617
1437
891
810
756
1650
158 |
| HKADN56 | 968619 | 590 | HMMER
1.8 | PFAM: Phorbol esters /
diacylglycerol binding
domain | PF00130 | 5.32 | 207 | 233 |
| HKIXG58 | 464241 | 591 | HMMER
1.8 | PFAM: Phorbol esters /
diacylglycerol binding
domain | PF00130 | 3.59 | 84 | 137 |
| HILIC113 | 626559 | 592 | HMMER
1.8 | PFAM: Phorbol esters /
diacylglycerol binding
domain | PF00130 | 4.83 | 328 | 378 |
| HILTGF17 | 662405 | 284 | HMMER
1.8 | PFAM: Phorbol esters /
diacylglycerol binding
domain | PF00130 | 3.46 | 136 | 183 |
| HLYDC50 | 1151494 | 285 | blastx.14 | similar to C.elegans
protein (Z37093) [Homo
sapiens] | gi 1504026 dbj BAAI
3212.1 | 59%
52%
37% | 275
719
32 | 652
871
127 |

| | | | | | | | | |
|----------|---------|-----|--------------|---|-------------------|-------|------|-----|
| HL YDC50 | 677050 | 593 | HMMER
1.8 | PFAM: Phorbol esters /
diacylglycerol binding
domain | PF00130 | 29.67 | 191 | 319 |
| HMADD49 | 1217031 | 286 | blastx.14 | L-aspartate oxidase (EC
1.4.3.16) nadB [validated]
-1 | pir E65035 OXECLD | 100% | 2212 | 803 |
| HMADD49 | 867481 | 594 | HMMER
1.8 | PFAM: Phorbol esters /
diacylglycerol binding
domain | PF00130 | 3.79 | 131 | 175 |
| HMEKE78 | 792383 | 595 | HMMER
1.8 | PFAM: Phorbol esters /
diacylglycerol binding
domain | PF00130 | 3.04 | 3 | 35 |
| HMSHU26 | 681745 | 596 | HMMER
1.8 | PFAM: Phorbol esters /
diacylglycerol binding
domain | PF00130 | 6.77 | 158 | 226 |
| HNEEB82 | 778884 | 597 | HMMER
1.8 | PFAM: Phorbol esters /
diacylglycerol binding
domain | PF00130 | 3.33 | 126 | 152 |
| HNHIA06 | 859932 | 598 | HMMER
1.8 | PFAM: Phorbol esters /
diacylglycerol binding
domain | PF00130 | 3.13 | 123 | 146 |
| HODFY16 | 958329 | 599 | HMMER
1.8 | PFAM: Phorbol esters /
diacylglycerol binding
domain | PF00130 | 3.15 | 175 | 213 |
| HPQSB68 | 740087 | 600 | HMMER
1.8 | PFAM: Phorbol esters /
diacylglycerol binding
domain | PF00130 | 3.9 | 170 | 247 |
| HRDBH04 | 922022 | 601 | HMMER
1.8 | PFAM: Phorbol esters /
diacylglycerol binding
domain | PF00130 | 5.19 | 600 | 632 |
| HSICR69 | 531061 | 602 | HMMER
1.8 | PFAM: Phorbol esters /
diacylglycerol binding
domain | PF00130 | 3.1 | 190 | 213 |

| | | | | | | | | |
|---------|---------|-----|----------------|---|------------------------------|----------------------------|--------------------------|----------------------------|
| HSIGJ94 | 793624 | 603 | HMMER
1.8 | domain
PFAM: Phorbol esters /
diacylglycerol binding
domain | PF00130 | 3.15 | 207 | 239 |
| HSYBL15 | 1104299 | 296 | blastx.14 | (AF021935) mytonic
dystrophy kinase-related
Cdc42-binding kinase
[Rattus norvegicus] | gi 2736151 gb AAC0
2941.1 | 94% | 2 | 931 |
| HSYBL15 | 660053 | 604 | HMMER
1.8 | PFAM: Phorbol esters /
diacylglycerol binding
domain | PF00130 | 22.31 | 2 | 70 |
| HTEKH29 | 855660 | 297 | HMMER
2.1.1 | PFAM: Phorbol
esters/diacylglycerol
binding domain (C1
domain) | PF00130 | 42.4 | 1660 | 1803 |
| HTGEL46 | 685425 | 605 | HMMER
1.8 | PFAM: Phorbol esters /
diacylglycerol binding
domain | PF00130 | 7.26 | 398 | 433 |
| HTGFA05 | 972982 | 606 | HMMER
1.8 | PFAM: Phorbol esters /
diacylglycerol binding
domain | PF00130 | 4.17 | 905 | 855 |
| | | | blastx.2 | phosphorylation
regulatory protein HP-10 -
human | pir A61382 A61382 | 99%
100%
74%
100% | 214
1080
827
67 | 909
1259
1078
213 |
| HTLDU61 | 530316 | 607 | HMMER
1.8 | PFAM: Phorbol esters /
diacylglycerol binding
domain | PF00130 | 5.45 | 102 | 125 |
| HTOFT34 | 527144 | 608 | HMMER
1.8 | PFAM: Phorbol esters /
diacylglycerol binding
domain | PF00130 | 4.53 | 235 | 264 |
| HTTDH46 | 1152491 | 302 | blastx.14 | F10B5.8 [Caenorhabditis
elegans] | gi 5824432 emb CAB | 74% | 32 | 607 |

| | | | | | elegans] | 54223.1] | 70% | 623 | 1144 |
|---------|---------|-----|----------------|--|--|--------------------------------|-------------|------------|------------|
| HTTDH46 | 951114 | 609 | HMMER
1.8 | | PFAM: Phorbol esters /
diacylglycerol binding
domain | PF00130 | 3.36 | 420 | 470 |
| | | | blastx.14 | | F10B5.8 [Caenorhabditis
elegans] | gi 5824432 emb CAB
54223.1] | 73%
73% | 117
2 | 437
124 |
| HTTIO05 | 931037 | 610 | HMMER
1.8 | | PFAM: Phorbol esters /
diacylglycerol binding
domain | PF00130 | 4.25 | 1289 | 1330 |
| HWHGY45 | 911621 | 304 | HMMER
1.8 | | PFAM: Phorbol esters /
diacylglycerol binding
domain | PF00130 | 10.67 | 123 | 203 |
| HWLQR48 | 914556 | 611 | HMMER
1.8 | | PFAM: Phorbol esters /
diacylglycerol binding
domain | PF00130 | 4.03 | 359 | 391 |
| HWLQX76 | 894607 | 612 | HMMER
2.1.1 | | PFAM: RhoGAP domain | PF00620 | 97.4 | 715 | 963 |
| HATDD09 | 1165331 | 307 | blastx.14 | | (AK000239) unnamed
protein product [Homo
sapiens] | gi 7020190 dbj BAA9
1027.1] | 52% | 3 | 260 |
| HATDD09 | 573794 | 613 | HMMER
1.8 | | PFAM: Cyclic nucleotide-
binding domain | PF00027 | 9.43 | 59 | 124 |
| HBJGT03 | 923800 | 614 | HMMER
1.8 | | PFAM: Cyclic nucleotide-
binding domain | PF00027 | 8.96 | 41 | 100 |
| HMTMF45 | 1141737 | 309 | blastx.14 | | (AL109657) dJ842G6.1
(novel protein) [Homo
sapiens] | gi 6691957 emb CAB
65791.1] | 96%
100% | 108
476 | 377
700 |
| HMTMF45 | 553382 | 615 | HMMER
1.8 | | PFAM: Cyclic nucleotide-
binding domain | PF00027 | 8.27 | 230 | 292 |
| HHPDV86 | 522953 | 310 | HMMER
2.1.1 | | PFAM: PH domain | PF00169 | 33 | 196 | 531 |

| | | | | | | | | |
|---------|--------|-----|-----------------------------|--|--|-----------------------------|-------------------------|---------------------------|
| HE8BT56 | 732602 | 311 | HMMER
2.1.1 | PFAM: Ras family | PF00071 | 46.1 | 138 | 248 |
| HUJDH06 | 907613 | 312 | HMMER
2.1.1
blastx.14 | PFAM: ADP-ribosylation
factor family
(AF143680) arf-like
protein 2 [Mus musculus] | PF00025
gi 4929218 gb AAD3
3908.1 AF143680.1 | 62.3
32%
48% | 433
421
264 | 669
663
356 |
| HOEJG61 | 907614 | 313 | HMMER
2.1.1
blastx.14 | PFAM: ADP-ribosylation
factor family
(AF031903) ADP-
ribosylation-like factor
homolog ARL6 [Mus
musculus] | PF00025
gi 3687625 gb AAC6
2194.1 | 45.6
75%
48% | 399
399
566 | 566
566
652 |
| HE8PN24 | 907620 | 314 | HMMER
1.8
blastx.14 | PFAM: ADP-ribosylation
factors (Arf family)
(contains ATP/GTP
binding P-loop) | PF00025
gi 727191 gb AAA64
266.1 | 104.77
38%
34% | 197
191
386 | 568
430
568 |
| HGBHI37 | 909745 | 315 | HMMER
2.1.1
blastx.14 | PFAM: PH domain
(AF017368) faciogenital
dysplasia protein 2 [Mus
musculus] | PF00169
gi 3599940 gb AAC3
5430.1 | 30.1
82%
63% | 107
14
145 | 259
151
201 |
| HCHOK82 | 909755 | 316 | HMMER
2.1.1
blastx.14 | PFAM: RhoGEF domain
(AF017369) faciogenital
dysplasia protein 3 [Mus
musculus] | PF00621
gi 3599942 gb AAC3
5431.1 | 176.8
90%
79%
100% | 40
31
855
1062 | 519
849
941
1082 |
| HFPCH24 | 912608 | 317 | HMMER
1.8 | PFAM: Ras family
(contains ATP/GTP
binding P-loop) | PF00071 | 43.25 | 47 | 307 |

| | | | | | | | | |
|---------|--------|-----|-------------|---|---------------------------|-------|-----|-----|
| | | | blastx.14 | rap2b gene product (AA 1-183) [Homo sapiens] | gi 35863 emb CAA37178.1 | 41% | 35 | 229 |
| HTTKF86 | 912689 | 318 | HMMER 2.1.1 | PFAM: Ras family | PF00071 | 29.6 | 98 | 223 |
| HCESA79 | 912709 | 319 | HMMER 2.1.1 | PFAM: Ras family | PF00071 | 45.1 | 67 | 243 |
| | | | blastx.14 | (AB027137) RAB-26 [Homo sapiens] | gi 5931612 dbj BAA84707.1 | 92% | 52 | 246 |
| HDTBJ28 | 912714 | 320 | HMMER 2.1.1 | PFAM: Ras family | PF00071 | 28.1 | 21 | 137 |
| | | | blastx.14 | Rab12 protein [Canis familiaris] | gi 437985 emb CAA80471.1 | 88% | 21 | 98 |
| HDPBF48 | 912783 | 321 | HMMER 2.1.1 | PFAM: Ras family | PF00071 | 26.1 | 33 | 101 |
| | | | blastx.14 | (AL117204) predicted using Genefinder [Caenorhabditis elegans] | gi 5832782 emb CAB55120.1 | 48% | 123 | 209 |
| | | | | | | 55% | 258 | 338 |
| | | | | | | 68% | 33 | 89 |
| | | | | | | 53% | 429 | 467 |
| HTPFY55 | 912928 | 322 | HMMER 2.1.1 | PFAM: Ras family | PF00071 | 27.2 | 240 | 386 |
| | | | blastx.14 | similar to the RAS gene family [Caenorhabditis elegans] | gi 572819 gb AAB09163.1 | 48% | 117 | 383 |
| | | | | | | 60% | 396 | 524 |
| HMSCM47 | 923632 | 323 | HMMER 2.1.1 | PFAM: ATPases associated with various cellular activities (AAA) | PF00004 | 121.1 | 65 | 652 |
| | | | blastx.2 | (AF033862) Lon protease [Arabidopsis thaliana] | gb AAC05085.1 | 65% | 5 | 673 |
| HEOQA56 | 925132 | 324 | HMMER | PFAM: Ras family | PF00071 | 62.8 | 53 | 154 |

| | | | 1.8 | (contains ATP/GTP binding P-loop) | | | | |
|---------|--------|-----|--------------------------|--|--------------------------------------|---------------------------------|--------------------------------|----------------------------------|
| HTPCQ24 | 925349 | 325 | blastx.14
HMMER 2.1.1 | GTP-binding protein [Discopyge ommata]
PFAM: PH domain | gi 213115 gb AAA49230.1
PF00169 | 76% | 23 | 202 |
| HWAEI37 | 929481 | 326 | HMMER 2.1.1
blastx.14 | PFAM: MCM2/3/5 family
(AL035461) dJ967N21.5 (novel MCM2/3/5 family member) [Homo sapiens] | PF00493
gi 5834569 emb CAB55276.1 | 31
59.7
100%
92% | 217
8
323
2 | 438
415
415
85 |
| HDPSF03 | 969536 | 327 | HMMER 2.1.1
blastx.14 | PFAM: ATPases associated with various cellular activities (AAA) | PF00004 | 47.2 | 61 | 399 |
| HLHST63 | 581528 | 328 | HMMER 2.1.1 | LON1 protease [Zea mays] | gi 1816586 gb AAC50011.1 | 58%
62%
41%
36%
30% | 46
865
622
580
642 | 447
1200
846
636
710 |
| HFAAJ44 | 489201 | 329 | HMMER 2.1.1 | PFAM: Ras family | PF00071 | 30.6 | 213 | 85 |
| HSLEM44 | 506604 | 330 | HMMER 2.1.1 | PFAM: Rhomboid family | PF01694 | 49.5 | 6 | 299 |
| HETCL79 | 522826 | 331 | HMMER 2.1.1 | PFAM: AcrB/AcrD/AcrF family
PFAM: PDZ domain (Also known as DHR or GLGF). | PF00873
PF00595 | 137.4
28.1 | 2
242 | 256
457 |
| HFTAR20 | 670041 | 332 | HMMER 2.1.1 | PFAM: Glypican | PF01153 | 170.7 | 12 | 308 |
| HCUFD32 | 699379 | 333 | HMMER | PFAM: PDZ domain | PF00595 | 29.3 | 124 | 369 |